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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm n.a. Srch_nn

Thu Apr 29 02:55:57 1999; MasPar time 500.39 Seconds 1416.800 Million cell updates/sec not generated. Tabular output Run on:

ggctggagaagaacagcaa......atagctgtgaagacacagaa 300 ccgacctctttttgtcgtt......tatcgacacttctgtgtctt 1 ggctggagaagaaacagcaa. >US-08-968-800-1 (1-300) from US08968800.seq 299 Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 602357 seqs, 1181590623 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

emb157 Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_vi genbank110 16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi Database:

Mean 9.536; Variance 4.385; scale 2.175 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	~	m	ю	_	m	m	m	m	~	~	~	~	~
Pred. No.	5.68e-22	1.76e-08	4.69e-05	9.58e-04	4.18e-03	4.18e-0	4.18e-03	4.18e-0	1.78e-02	1.78e-02	1.78e-02	1.78e-02	1.78e-02
Description	Sequence 14 from paten	Sequence 5 from patent	Homo sapiens chromosom	Sequence 22 from paten	Sequence 5 from patent	Human TAN-1 mRNA (homo	Human DNA sequence ***	Homo sapiens Chromosom	Sequence 22 from paten	Mus musculus bone morp	M.musculus notch-1 mRN	R.rattus mRNA homologu	Homo sapiens chromosom
TD	166494	128278	AC005369	AR024229	128278	HUMTAN1	HS329A5	HUAC004787	AR024229	MUSBMP1A	MMNOTCHA	RRNOTCH	AC005369
DB	22	22	27	22	22	56	18	27	22	29	53	59	27
% Query Match Length DB	7218	215	74371	965	215	7332	183338	216021	965	2976	8064	8221	74371
% Query Match	17.7	11.7	10.0	9.	0.6	0.6	0.6	0.6	8.7	8.7	8.7	8.7	8.7
Score	53	35	30	28	27	27	27	27	26	26	26	26	56
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7.37e-02 7.37e-02 7.37e-02	.37e	.37	.37	7.37e-02 7.37e-02	w. w	.37e	7.37e-02	w. r	376	7.37e-02	.37	'n	9	m.	.37	m.	.37€	ĸ,	.37	.37	'n	.37	7.37e-02
gDNA encoding envelope Human cDNA encoding a gDNA encoding a peptid	nce 6 from ragment nam	8 from	Sequence 7 from patent gDNA encoding a peptid	타영	Sequence 23 from paten	human	Ę,	Human cDNA encoding a	DNA encoding recombina	g a pep	human	DNA encoding human thr	g thromb	NA encodi	1 from F		DNA n	from	E	D.melanogaster dorsal-	Human thrombomodulin D	Human thrombomodulin g	Homo sapiens gene for
E04076 E12212 E09438		184564 120813	I84563 E09434	E12213 E03192	I20828 F08243	E08242	146801	E12209	E03193	E09440	E08244	E08245	E09580	E12211	101906	186964	E09545	I20815	I84566	DRODVP	A01561	HUMTHMA	номтм
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c 14 15	17	100 E	21 22	23 24	25 25	27	28	50	316	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

166494 7218 bp DNA Sequence 14 from patent US 166494 92724471 Unclassified. Unclassified. 1 (bases 1 to 7218) Unclassified. 1 (bases 1 to 7218) Dorner,F., Scheifinger,F. Recombinant fowloave virus Patent: US 5670367-A 14 23. Location/Qualified. 1. 7218 1. 7228 1	1 1 1 1 1 1 1 1 1 1	from patent US 5670 from		Query Match 17.7%; Score 53; DB 22; Length 7218; Best Local Similarity 0.3%; Pred. No. 5.68e-22; Matches 1; Conservative 173; Mismatches 122; Indels 0; Gaps 0;	TYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
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US-08-968-800-1.rge

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DOE Joint Genome Institute.
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Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                                                                                                                                                 1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 556980-A 5 29-OCT-1996;
Location/Qualifiers
120 gcaggitticccggigiatcciggaaagcaictgcaittgittggicccacgcactcacc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 ctgtgtcttcacagctatactgacagtttatcatggca-catgtcctngagttcacacac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 qtagcatctggcatgagcatgtggccactgaggcaaaagcacttgtagcttccgtgtgta 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 VNNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 74471)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Radner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Sequencing of human chromosome 5
Upublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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3 (bases 1 to 74371)

Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.,
Rojeski, H., Subramanian, S. and Martin, C.H.

Direct Submission
Submitted (01-AuG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                aaacttacatccaggttcgcatgtagcttcacagactcccttgctgtttcttctcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 22; Length 215;
Pred. No. 1.76e-08;
64; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     141 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 KNNGDRNNRYGTGTKSNVSNNCGGGNKRDVSSYANNKCCGSSCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 ttc-acacatctgtgttggcatggccgggggtttcattccacact 137
                                                                                                                                                                                                                                                                                                                                                                                                               26 t
                                                                                                                                DEFINITION Sequence 5 from patent US 5569830.
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8 c 25 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 17.1%;
Matches 28; Conservative
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AC005369
93367505
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                                                                                                                                                                                                                      Unknown.
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ORGANISM
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complement(join(38063. .38218,38462. .38578,38741. .38995,39071. .39205,39532. .39630,39935. .40048,40300. .40410,40503. .40661,41868. .41972,42103. .42225,42492. .42569,
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name="histidy1-tRNA synthetase"
/note="78%-100% protein identity GenPept:U18937"
complement(38069. :38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. :38578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 22; Length 965;
Pred. No. 9.58e-04;
50; Mismatches 44; Indels 0;
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0
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Pred. No. 4.69e-05;
46; Mismatches 36; Indels 0
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                                                                                       /note="GRAIL 2 excellent exon, frame 2" complement(35238. .35331)
/note="GRAIL 2 excellent exon, frame 1" 36392. .36663
                                                                                                                                                                                                                                                                                                                                                                                     frame 0"
                                                                                                                                                                                    /rpt_family="Alu"
36901. 37222
/note="100% identity EST ou55c09.x1"
/db_xref="dbEST:AI025011"
36901. 37164
/standard_name="STSG-9983"
/db_xref="dbSTS:G26554"
complement(37595. 37654)
/note="GRAIL 2 excellent exon, frame 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 16127 SSSYCKSCCWMMSWRMKKGSWKKRMWWRCRWGMGYSASCSAS 16168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 cggccatgccaacacagatgtgtgaatacacacggaagctac 195
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Sequence 22 from patent US 5795961.
AR024229
93977523
/rpt_family="MLT1"
complement(33670. .33785)
/rpt_family="Alu"
                                                                      complement(34021. .34144)
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170 c 226 g
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Best Local Similarity 19.6%;
Matches 20; Conservative
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Best Local Similarity 14.5%;
Matches 16; Conservative
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Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata: Eutheria; Primates; Catarrhin; Hominidae; Homo. I (bases I to 7332)
Ellisen,L.W., Bird,J., West,D.C., Soreng,A.L., Reynolds,T.C., Smith,S.D. and Sklar,J.
TAN-I, the human homolog of the Drosophila notch gene, is broken by chromosomal translocations in I lymphoblastic neoplasms 91347367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:9338675"
/translation="MPPLLAPLLCLALLPALAARGPRCSQPGETCLNGGKCEAANGTE
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YVPCSPSPCQNGGTCRPTGDVTHECACLPGFTGQNCEBNIDDCPGNNCRNGGACVDGV
NTYNCPCPPEWTGQYCTEDVDECQLMPNACQNGGTCHNTHGGYNCVCVNGWTGEDCSE
NIDDCASAACFHGATCHDRVASFYCECPHGRTGLLCHLNDACISNPCNEGSNCDTNPV
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                                                                                                                              Unclassified.

(bases 1 to 215)

Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to
control fungal disease
Patent: US 5569833-A 5 29-00T-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                     92 KIVIDSYNASGISSSNGGIDGNRSG-ADSYGSSKTAMISRNRIGKIANNAVDSRNMGDAS 150
                30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMTANI 7332 bp mRNA PRI 13-JAN-1995
Human TAN-1 mRNA (homologue of Drosophila Notch gene), 5' end.
M73880
9338674
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Pred. No. 4.18e-03;
51; Mismatches 45; Indels
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128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
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1. 733
7. 733
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Jurkat"
/map="9934.3"
/gene="TANI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="GDB:G00-131-400"
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Best Local Similarity 14.0%;
Matches 16; Conservative
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/partial
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YETAKVLLDHFANRDITDHMDRLPRDIAQERMHHDIVRLLDEYNLVRSPQLHGAPLGG
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LLDSSGMLSPVDSLESPHGYLSDVASPPLLPSPFQQSPSVPLNHLPGMPDTHLG1GHL
NVAAKPEMAALGGGGRLAFETGPPRLSHLPVASGTSTVLGSSSGGALNFTVGGSTSLN
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5;
297832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQQSLQPPPPPPPPHLGV
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Pred. No. 4.18e-03;
0; Mismatches 15; Indels
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1374 a 2545 c 2268 g 1
Chromosome g34.3.
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Best Local Similarity 73.7%;
Matches 42; Conservative
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HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 965)
Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -, Homo sapiens"
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                                                                                                                                                                        27765. .27872
/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -, Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="dbSTS:G02122"
175801. 175945
//db_xref="16084, CHC.GCT10B02, Chr. -, Homo sapie:
//db_xref="dbSTS:G09703"
175810. 175945
//note="1616, CHLC.GCT15C04, Chr. -, Homo sapie:
//db_xref="dbSTS:G09935"
199463. 199572
//db_xref="dbSTS:G09935"
//db_xref="dbSTS:G04338"
//db_xref="dbSTS:G04338"
//db_xref="dbSTS:G04338"
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//db_xref="dbSTS:G04338"
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Pred. No. 4.18e-03;
60; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| : |::: ::|:: :::| :| :| :| : : : :::| :: |:: |:: |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: | |:: |:: |:: |:: | |:: |:: |:: |:: | |:: |:: |:: | |:: |:: | |:: |:: | |:: |:: | |:: | |:: |:: | |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: 
                                                                                                                                                                                                                                                                          /db_xref="dbsTs:G02280"
73826. .73943 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1493 YCMGRAMMAAAWYYKRRSCMAWYYYMRGRARKTYYYMARRRGCARSYK 1540
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Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualifiers
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Pred. No. 1.78e-02;
54; Mismatches 44;
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from patent US 5795961
          /organism="Homo sapiens"
                                      /db_xref="taxon:9606"
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170 c 226 g
                                                                                                                                        /clone="A-952F10"
27765. .27872
                                                                      /chromosome="16"
/map="#16q21-22"
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Best Local Similarity 9.3%;
Matches 10; Conservative
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Local Similarity 15.4%;
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Sequence 22 f
AR024229
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Submitted (24-JUL-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Medical Center Dr., Rockville, MD 20850, USA

On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgenetigr.org. The orientation of the sequence is from SP6 end to T7 end Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html). Genes without peptide homolgy having spliced EST hits are termed 'Unknown gene product', Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).

Location/Qualifiers

Lice 1. 216021
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HOMO Sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
sequence.
2002 bp Unfinished: dJ329A5 Contig_ID: 03639 acc=297832 Length: 55652 bp Unfinished: dJ329A5 Contig_ID: 04239 acc=297832 Length: 21109 bp Unfinished: dJ329A5 Contig_ID: 03867 acc=297832 Length: 2332 bp Unfinished: dJ329A5 Contig_ID: 00527 acc=297832 Length: 96075 bp Unfinished: dJ329A5 Contig_ID: 04002 acc=297832 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216021)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo, Sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                          * This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       *** WARNING: Phase 1 High Throughput Genome Sequence ***
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Adams, M.D. and Loftus, B.J.
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Best Local Similarity 73.7%;
Matches 42; Conservative
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93337381
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RESULT

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DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS SFERENCE AUTHORS TITLE JOURNAL

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FEATURES

SE COUNT

04-DEC-1998

MEDLINE REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

TITLE

JOURNAL

TITLE

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L (Dases 1 to 29/0)

Fukagawa,M., Noboru,S., Hogan,B.L.M. and Jones,C.M.
Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1)
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astain metalloproteinase
Dev. Biol. 163, 175-183 (1994)

94229342.
On Jan 6, 1994 this sequence version replaced gi:437434.
L. 2976
//organisma-Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELGHVIGEWHEHTRDDER YLYFT RPCGCCSYVGRGGODALSTGKNCNKFGIVH
ELGHVIGEWHEHTRDDER YLYFT RPCGCCSYVGRGGODALSTGKNCNKFGIVH
ELGHVIGEWHEHTRDDER HYSIVFEN FLORGCSYVGRGGODALSTGKNCNKFGIVH
YARRTFSRGIFLDI YVPK YEVNGVKPSIGORTRLSKGDI-AQARKIYKCPAGGETLQDS
TGNFSSPELP HOGSSAIMHCWRISVTPGEK IILNFTSMDLYRSRLCWYDYVEVRDGFW
IOSPNYPDDYRRSKYGHRIOVSEGFHVGLFROSFEI ERHDSCAYDYLEVDGHSESS
NLIGRYCGYENPDDIKSTSSRLWLKFVSDGSINKAGFANNFFKEVDECSRPNRGGED
RCLNTLGSYKCSCDGGYELDARLKFVSDGSINKAGFANNFFKEVDCSRPNRGGED
OLVAPTOYRISLOPPFFFTGGNDVCKYDFVEVRGSTALNGSITSGGNER FFINSOL
      Mus musculus bone morphogenetic protein (Bmp-1) mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:g439607"
/translation="MPGVARPPLPLISLPLLLLLLLLPARRPAAGLGRLHLRPGRGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGAPOLORPLOGGCLPWDIALDEEDLRAFOVOQAAVLROOTARRPSIKAAGNSSALGG
QGTSGOPORESRGRWRGRPRSRRAATSRPERVWPDGVIPFVIGGNFTGSORAVFRQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNNMRVEFKSDNTVSKKGFKAHFFSDKDECSKDNGGCOODCYNTFGSYECOCRSGFVL
HDNKHDCKEAGCEHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHRVKLTFVEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQASHSTECGGQVRADVKTKDLYSHAQFGDNNYPGGVDCEWVIVAEEGYGVELVFQTF
EVEEETDCGYDYIELFPGYDSTAPRLGRYCGSGPPEEVYSAGDSVLVKFHSDDTISKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I ESQPECAYDHLEVFDGRDAKAPVLGRFCGSKKPEPVLATGNRMFLRFYSDNSVQRKG
                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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0
                                     9439606
bone morphogenetic protein-1; metalloproteinase.
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Pred. No. 1.78e-02;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="bone morphogenetic protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'dev_stage="embryo"
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211886 S47228
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Best Local Similarity 72.4%;
Matches 42; Conservative
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1 (bases 1 to 8064)
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                                                                                                                                                                         Murinae; Mus.
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                                                                                                         ORGANISM
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AUTHORS
TITLE
                   ACCESSION
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COMMENT
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ORGANISM
                                                             KEYWORDS
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del Amo, F.F., Gendron-Maguire, M., Swiatek, P.J., Jenkins, N.A., Copeland, N.G. and Gridley, T. Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch Genomics 15 (2), 259-264 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MPRLLTPLLCLTLLPARAARGLRCSQPSGTCLNGGRCEVASGTE"
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-APR-1992) Thomas Gridley, Dept. of Cell and
Bevelopmental Biology, Roche, Institute of Molecular Biology, 340
Kingsland Street, Nutley, NJ, 07110-1199, USA
3 (bases 1 to 8064)
Cuintek, P.J., Gendron-Maguire, M.,
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VCAVASNTARGFICRCPAGFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACVASGSFVGQRCQDPNPCLSTRCKNAGTCYVVDHGGIVDYACSCPLGFSGPLCLTPI
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GPDIPPPQIEEACELPECQVDAGNKVCNLQCNNHACGWDGGDCSLNFNDPWKNCTQSL
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ECEWDGLDCAEHVPERLAAGTLVLVVLLPPDQLRNNSFHFLRELSHVLHTNVVFKRDA
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EIDNROCVOSSSOCFOSATDVAAFLGALASLGSLNIPYKIEAVKSEPVEPPLSSGLHI
MYVAAAAFVLLFFVGGGVLLSRKRRRQHGQLWFPEGFKVSEASKKKRREPLGEDSVGL
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DSLESPHGYLSDVASHPLLPSPFQQSPSMPLSHLPGMPDTHLGISHLNVAAKPEMAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="homologue of Drosophila neurogenic gene Notch"
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Location/Qualifiers
1. .8064
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/dev_stage="embryonic day
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/product="notch-1"
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/db_xref="PID:e1291872"
/db_xref="PID:93123945"
/tanslation="MPRLIAPLILIPALAARGLRCSQPSGTCLNGGRCEVANGTE
ACVCSGAFVGQRCQDPSPCLSTPCRNAGTCYVVDHGGIVDYACSCPLGFSGPLCLTPL
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TGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPGFTGSYCQYDVNECDSRPC
GWVPSQYNPLRPGVTPGTLSTQAAGLQHSMMGPLHSSLSTNTLSPIIYGLPNTRLÄT
OPHLVQTQVQVQPQNLPLQDQNLQPSQPHLSVSSAANGHIGKSFLSGBPSQANVQPLG
PSSLPVHTILPQESQALPTSLPSNMPPMTTQFLTPPSQHSYSSSPVDNTPSHQLQV
PEPTFLTPSPESPPOMSSSSPHSNISONSEGISSPPTTMPSQIIHIPEDRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-APR-1998) G. Weinmaster, Salk Institute, Molecular Neurobiology Laboratory, San Siego CA 92186, U S A On May 8, 1998 this sequence version replaced g1:57634.
                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                       Length 8064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          лкиотСН 8221 bp mRNA ROD 06
R.rattus mRNA homologue of Drosophila notch protein.
X57405
                                                                                                                                                                                                                                                                           Score 26; DB 29; Length 806.
Pred. No. 1.78e-02;
0; Mismatches 16; Indels
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1 (bases 1 to 8221)
Weinmaster, G., Roberts, V.J. and Lemke, G.
                                                                                                                                                             1668 t
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241. .7836
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                                                                                                                                                             2218 g
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Weinmaster, G.
Direct Sure.
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Weinmaster, G.
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.4%;
Matches 42; Conservative
                                                                                                                                                             2439 c
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GORDMIEPYYGREEELRANDINAMETERIAGINEN TEATHORY TO THE TRANSPORT OF THE TRANS
                                                                           VCAVASNTARGFICRCPARFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGSF
TGPECOFPASSPCVGSNPCYNOGTCEPTSESPFYRCLCPAKFNGLLCHLLDYSTTGAA
GRDIPPPQIEBACELPECQEDAGNYCNLQCNNHACGWDGGCSLNFNDPWKNCTQSL
QCWYFSDGHCDSQNSAGCLEDGEDCQLTEGQCNPLYDQYCKDHFSDGHCDGGCNS
ECEWDGLDCARHYDFRLAAGTLVLVVLLLPPQDLRNNSFHELRDVSHVLHTNVVFKRDA
YKCSCPRGTQGVHCEINVDDCHPPLDPASRSPKCFNNGTCVDQVGGYTCTCPPGFVGE
RCEGDVNECLSNPCDPRGTQNCVQRVNDFHCECRAGHTGRRCESVINGCRGKPCRNGG
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PSSLPVHTILPQESQALPTSLPSSMVPPMTTTQFLTPPSQHSYSSSPVDNTPSHQLOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMVPSQYNPLRPGVTPGTLSTQAAGLQHGMMGPIHSSLSTNTLSPIIYQGLPNTRLAT
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Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74371)
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DoE Joint Genome Institute.
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Pred. No. 1.78e-02;
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Best Local Similarity 73.2%;
Matches 41; Conservative
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'db_xref="taxon:9606"

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repeat_region
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complement(7830, .8185)
Standard_name="possible repeat"
8258, .8503
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/rpt.family="Alu"
Complement (16993, .17085)
/rpt_family="MER42"
Complement (17678, .18276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(9740. .9845)
/rpt_family="MER42"
complement(10440. .11015)
/rpt_family="Alu"
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6586. .6956
/rpt_family="L1"
6647. .6684
/note="(CA)19"
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3707. 3728
/note="(A)22"
/rpt_type=tandem
/rpt_unit=A
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5327. .5602
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12057. .12085
/note="(A)29"
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/rpt_unit=A
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14175. 14470
/rpt_family="Alu"
complement(14906.
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070. .9387
rpt_family="Alu"
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13727. .13750

Mote="(AC)12"

Tpt_type=tandem

rpt_unit=AC
13783. .14024
                                                                                                                                                                                                                                                                                                                                              rpt_type=tandemrpt_rpt_unit=cA
             /chromosome="5"
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6671. 1660
/clone="119j3"
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fpt_unit=T
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note="(T)20"
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/rpt_family="%lu"

join(29485. .29559,29598. .29779)

/note="85% identity dbsTs:G14522 (SHGC-11312)"

/standard_name="A1027942"

/note="100% identity EST ov84a10.x1"

complement(30401. .30536)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28712. .28930
/rpt_family="MER20"
complement(28769. .28838)
700# 26821L 2 excellent exon, frame 0"
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/note="GRAIL 2 excellent exon, frame 2"
complement(35238. .35331)
                                                                                                                                                                                                                                                                                                         /standard_name="possible repeat"
23022. 23326
/rpt_family="Alu"
23473. 23761
/rpt_family="Alu"
23744. 23767
/note="(A)24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(24639. 24694)
/rpt_family="MER42"
complement(25349. 25713)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                .22981)
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                                                                                                                                 21202. .21496
/rpt_family="Alu"
21736. .22035
/rpt_family="Alu"
22017. ??^?
Trpt_family-"Alu"
19305. 19583
/rpt_family-"Alu"
19914. 19948
/rote-"(GTT)8"
/rpt_type-tandem
/rpt_unit-GTTY
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7774. .28057
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/rpt_family="Alu"
complement(22638.
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28040. 28066
/note="(A)27"
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1202 21496
                                                                                                         complement (19943
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2977. .33088
rpt_family="MLT1"
                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_type=tandem
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2617. .32908
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8712
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Job time
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SOURCE
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                       Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
1 (bases 1 to 565)
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VICEBIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
AND METHOD FOR DETECTING THE SAME
PATENT: JP 1992349885-A 1 04-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          E04076 565 bp RNA PAT 26-NOV-1996

GDNA encoding envelope region of type C hepatitis virus.

E04076
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                                                                                                                                                                                    /standard_name="histidyl-tRNA synthetase"
/note="78%-100% protein identity GenPept:U18937"
complement(1806% .38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. .38578)
                                                                                                                                                                                                                                                                                                                                                                                             Db 15981 SGKKYWCRCSMYWYTCYYSYKYYWSMSYCTCTSWGWRWMWSKGRSWMYASRSG 16033
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Pred. No. 1.78e-02;
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                                                                                                                                                                                                                                                                                                                   64; Mismatches 40; Indels
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Pred. No. 7.37e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hepatitis C virus"
/db_xref="taxon:11103"
93 c 107 g 85 t
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Best Local Similarity 28.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 7.1%;
Matches 8; Conservative
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JP 1992349885-A/1.
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Hepatitis C virus
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DEFINITION
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YAMAMOTO SHUJI, SUZUKI KOJI
PC CO7H21/04, A61K38/00, C12N15/09, C12P21/02, (C12P21/02, C12R1:91);
CC strandedness: Double;
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1. .816
/product='Soluble thrombin binding protein'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAVING ACTION PROMOTING
                                                                                                                                                                                                                                                                                                                                                                                                                                              E12212 816 bp DNA PAT 27-APR-1998 Human cDNA encoding a soluble thrombin binding protein by which stimulates protein C activation.
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PN JP 1996291193-A/5
PD 05-NOV-1996
PF 08-JAN-1988 JP 1996138587
PR 08-JAN-1987 JP 87P 1065, 08-JAN-1987 JP 87P 1066,
11-JUN-1987 JP 87P 144081, 04-DEC-1987 JP 87P 305876, PR
04-DEC-1987 JP 87P 305877, 04-DEC-1987 JP 87P 305878 PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Districts, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 816)

Yamamoto, S. and Suzuki, K. .

MEDICINAL COMPOSITION CONTAINING PEPTIDE HAVING ACTION PROMOTY ACTIVATION OF PROTEIN C BY THROWBIN
PATENT: JP 1996291193-A 5 05-NOV-1996;
ASAHI CHEM IND CO LID
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                                                                                                                                               272 GGGYRGCGCTBACYC-CCACGSTYGCVRCYAGRRAYVBYAVYVTYCCCRC 320
                                                                                                                                                                                             Length 816;
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Pred. No. 7.37e-02;
0; Mismatches 25; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
297 c 248 g 135
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ilarity 66.7%;
Conservative
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JP 1996291193-A/5.
Homo sapiens.
Homo sapiens
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212 YVATCMTGCWYDYYCCBGGGTGYRYBCCYTGYGTYCGSGARRRYRRYNYTCBMGNTGYT 271

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 n.a. database search, using Smith-Waterman algorithm п.а. srch_nn qu ou:

Sat Apr 24 22:26:11 1999; MasPar time 60.26 Seconds 677.328 Million cell updates/sec not generated. Tabular output

>US-08-968-800-1 (1-300) from US08968800.seq 299 Title:

1 ggctggagaagaaacagcaa.......atagctgtgaagacacagaa 300 ccgacctcttctttgtcgtt.......tatcgacacttctgtgtgtctt Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Scoring table:

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188442 seqs, 68026449 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq32 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 7.783; Variance 4.414; scale 1.763 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.16e-11	1.16e-11	8.71e-10	8.71e-10	9.60e-07	9.60e-07	1.46e-05	1.46e-05	5.60e-05	5.60e-05	7.85e-04	7.85e-04	1.03e-02
Description	Base substituted E.co	Base substituted E.co	Oligonucleotide probe	Oligonucleotide probe	Generic DNA sequence	Generic DNA sequence		Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	DNA	Generic DNA sequence	Generic DNA sequence
ID	N81164	N81164	051746	Q51746	070469	070468	070465	070467	070470	070466	070465	070468	070469
80	н	~	σ	0	12	12	12	12	12	12	12	12	12
Suery Match Length DB	204	204	91	91	114	114	114	114	114	114	114	114	114
Query Match	13.4	13.4	12.4	12.4	10.7	10.7	10.0	10.0	9.7	9.7	0.6	0.6	8.4
Score	40	40	37	37	32	32	30	30	29	29	27	27	25
Result No.	п	7	m	4	Ŋ	9	7	ω	σ	10	11	12	13
Res		ပ		O	U	O	U	O	O	ပ			

108 Others;

11 T;

17 G;

47 C;

21 A;

1.03e-02 1.03e-02	1.03e-02	m	1.03e-02	1.03e - 02	1.03e - 02	1.03e - 02	1.03e-02	1.03e-02	1.03e - 02	1.03e - 02	1.03e-02	1.03e - 02	1.03e-02	1.03e-02	1.03e-02	3.63e-02	3.63e-02	3.63e-02	3e-		1.25e-01								
Generic DNA sequence Generic DNA sequence	nce encoding t	encoding	encoding	Sequence encoding thr	ಹ	Sequence encoding thr	Sequence encoding thr	Encodes truncated hum	Encodes thrombomoduli	cDNA encoding a human	Encodes thrombomoduli	Soluble thrombomoduli	Thrombin-binding subs	Encodes thrombomoduli	Recombinant thrombin-	Human thrombomodulin	Human thrombomodulin	Sequence encoding thr		coding	Sequence of human thr	2.1	Hind III - Not I thro	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	ric DN	DC43 TSAR library gen	Human IL-8 receptor-a
Q70467 Q70472	005947	005948	7	005945	T14656	005971	005973	020811	095956	T14654	095958	010435	013406	095957	025279	T12792	036458	005944	020810	N80892	N81065	N82026	048213	970466	970470	970473	970471	36	T76368
12	7, 1	Н.	-		N				н	$^{\circ}$	н			н		\sim								Н	н	Н	12	2	32
114	720	726	747	759	825	825	831	1425	1482	1491	1529	1545	1656	1680	1680	1946	2011	2313	2463	3373	3573	3640	6977	114	114	114	114	81	140
8 8 9 4 4 4		•		8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4				8.0		7.7
25	52.0	52	22	25	25	25	25	52	25	52	52	22	25	52	52	52	22	52	25	22	22	52	52	24	24	24	54	53	23
151	17	18	13	50	21	22	23	24	22	56	27	28	53	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45
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ALIGNMENTS

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7. 30 MAR-1988; 105163.
7. 810-MAR-1988; 105163.
7. 10 Introducing random point mutations into nucleic acods -
7. 10 Introducing random point mutations into nucleic acods -
7. 10 Introducing random point mutations were introduced into the alpha fragment of
8. 10 Introducing to manage in the meaning a primer, elongation,
8. 10 Introducing stranded template and an oligonucleotide was hybridised to
8. 11 to generate a popn of DNA molecules which terminate at all
8. 11 to generate a popn of DNA molecules which terminate at all
8. 11 to generate a popn of NNA molecules which errainate at all
8. 12 coli beta-galactosidase within a specified region. The
8. 12 transcriptase and the molecules are misincorporated by the
8. 12 transcriptase and the molecules are misincorporated by the
8. 13 transcriptase and the molecules are completed to forms that can be
8. 14 the sequence covers all 176 difft base substitutions, most of which
8. 15 to the sequence covers all 176 difft base substitutions, most of which
                                  N01164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                    /function=multiple cloning site 187..204
/*tag= b
                 standard; DNA; 204 BP.
                                                                                                                                                                        ø
                                                                                                                                                   19..69
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also P80575.
Sequence 204 BP;
                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                              EP-285123-A
                                                                                                                                                                                                                                                                   05-MAY-1988
                                                                                                                                                                                                         primer_bind
 LT 1
N81164
RESULT
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EP-571911-A

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WPI: 88-27992740.

Thirducing random point mutations into nucleic acods -

Thy prepn of single stranded template, annealing a primer, elongation, or standard template, annealing a primer, elongation, or standard template, annealing a primer, elongation, or standard template of molecules and screening.

S Disclosure; p; English.

S Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all consible nucleotide positions within a specified region. The rerest transcriptase and the molecules are misincorporated by the transcriptase and the molecules are completed to forms that can be malified and them expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                   78 dchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyv 137
                                                                                              87 mrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvh 146
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 cactcattcacatcttgactgcaggttttcccggtgtatcctggaaagcatctgactttg 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 T; 108 Others;
                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
         Length 204;
                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 40; DB 1; Length 204; Larity 9.2%; Pred. No. 1.16e-11; Conservative 53; Mismatches 36; Indels
                                                                                                                                         138 ybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhd 178
                                                                                                                                                                             174 tgtgaatacacacggaagctacaagtgcttttgcctcagtg 214
   Score 40; DB 1; L
Pred. No. 1.16e-11;
54; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                      19..69
/*tag= a
//uction=multiple cloning site
187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 nhnncncccbnnhvchnvhbnnhrnwayvrhdarrddv 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : ||| ::|: :: : |:: : |:::: | 80 tttggtccacgaactcaccaagttc 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 G;
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 C;
                                                                                                                                                                                                                                                  N81164 standard; DNA; 204 BP.
 Match 13.4%;
Local Similarity 11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 3
Q51746 standard; cDNA; 91 BP.
Q51746;
                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
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30-MAR-1988; 105163.
03-APR-1987; US-0348
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                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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Query Match
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                                   Matches
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ID Q5
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                                                                                                                                                                                                                                                                                                                   Gaps
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07-APR-1995 (first entry)
07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in samples
                                                                                                                                               Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of 101gonucleotide probe MK14-A consists of nucleotides 5-95 of 101335). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterials pp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 Bp; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligoniclectide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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                                                                                                                                                                                                                                                                                                                                                      31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                      New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                   10 gssvhsyyvvhvvshhhsvhhvvhhvhvvvhhvvhvvhhvhyhvysv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 9; Length 91;
Pred. No. 8.71e-10;
43; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%; Score 37; DB 9; Length 91; 2.0%; Pred. No. 8.71e-10; Vative 43; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 gssvhsyyvvhvvshhhsvhhvvhvsvvvvhhvvhvvhvhyhvyvsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 91 BP.
                                                          (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA;
                                                                                                                                                                                                                                                                            12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    070469 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                          1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Conservative
                          24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 14; 23pp;
                                                                                     WPI; 93-378844/48.
New oligo:nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1993; 108325
                                                                                                                                                                                                                                                                                          Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-571911-A.
                                                                                                                                       samples
Claim 3;
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Q51746 s
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misc_feature

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1993; US-176500.
1994; US-189331.
UNIV NORTH CAROLINA.
5 DM, KAY BK;
                 US-189331.
NORTH CAROLINA.
Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "this
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q70465 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                             10.7%;
imilarity 4.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                            0 A;
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WPI; 94-279739/34.
P-PSDB; R65150 and R65151.
US-013416.
US-176500.
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                                          WPI; 94-279739/34
P-PSDB; R65154.
                 31-JAN-1994; U
(UYNC-) UNIV N
FOWlkes DM, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994;
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31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DYNC-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random ISAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     //octs "this sequence represents 'Z'; Z can be a sequence of 6, 9 or 12 nucleotides (see comments)"
          ø
/*tag= a
/note= "this sequence represents 'Z'; Z can be
sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 nnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbt 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caaacttacatccaggttcgcatgtagcttcacagactcccttgctgtttct 10
                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.60e-07;
                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            4
G;
                                                                                                                                                                                                                                                                                                                                                                                              Score 32;
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                                                                                                                                                                                                                                                                                                                                                                            4
C,
                                                                                                                                                                                                                                                                                                                                                                  detection in a screening process.
Sequence 114 BP; 0 A; 4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .T 6
Q70468 standard; DNA; 114 BP.
Q70468;
                                                                                 31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                              10.7%;
8.0%;
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                           comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                              US-013416.
US-176500.
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01-FEB-1994; U00977.
                                                       U00977
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                             WPI; 94-279739,
                                                                01-FEB-1993;
                                                                       30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Screening a recombinant vector intrary expressing fusion proteins of screening a recombinant vector intrary expressing fusion proteins. Screening a recombinant vector intracts of 70468 is a generic DNA Sequence used to generate random TSAR (Totally CY 17048) is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be conditioned as follows: X(NNB)11(TGC)(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are conditioned for the same as Y) that are conditioned for the same as Y) that are conditioned by these generic sequences are shown in CYC 66-68. Other specific peptides generated by these generic sequences are shown in CYC 67-154. TSABS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a filmity for a ligand and a second effector peptide portion that is affinity for a ligand and a second effector peptide portion that is comprise a biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs or compens. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the conformation or in vivo antibody contains or polyclonal antibodies and therefore circumvent the need for composity are easily characterised and have designed activity process.
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
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5, 9 or 12 nucleotides (see
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Tdentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins by comprising a binding domain and an effector domain by bisclosure; Page 35, 255pp; English.

CC 070465 is a generic DNA sequence used to generate random TSAR (Totally comparing a period of the sequence used to generate formula can also be represented as follows: X(NNB) 12 (NNB) 14 (TGC) (NNB) 31. X and X are flanking restriction sites (X is not the same as Y) that are concatenated py these generic sequences are shown in 070466-68.

CC not specified further. Other generic sequences are shown in 070466-68.

CC comprising at least two functional proteins proteins or peptides, affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker chair the expressed peptide contains 2 or 4 cysteine residues positioned confer some degree of conformational rigidity to the peptides. The TSARs confer some degree of conformational rigidity to the peptides. The TSARs confer some degree of conformational rigidity to the peptides.

CC or compsns. comprising a TSAR binding domain can be used in vivo to radioisotope, peptide, toxin or enzyme, to the sepcific target or on the radioisotope, peptide, toxin or enzyme, to the sepcific target or on the radioisotope, peptide, toxin or enzyme, to the specific target or on the radioisotope, peptide, toxin or enzyme, to the specific target or on the component or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody complexed or complexed or complexed the function of macromolecules, ed.

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CC or complexed the designed and a specific activity allowing direct and rapid detection in a screening process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; synthetic.
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/*tote= "this sequence represents 'Z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
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Pred. No. 1.46e-05;
31; Mismatches 77; Indels
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US-176500.
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05-APR-1995
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01-FEB-1994;
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070467 is a generic DNA Sequence used to generate random ISAR (Totally Synthetic Affinity Reagents) peptides.This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)17. X

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35, 255pp; English.

WPI; 94-279739/34. R65153

P-PSDB;

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and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Cother specific peptides generated by these generic sequences are shown in CR65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is chemically or balogically active. They may further comprise a linker of peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned or in, or flanking, the unpredicted or variant residues. These residues comprises an engage of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to addistorbe, peptide, toxin or enzyme, to the specific target or on the conformational antibodies and therefore circumvent the need for monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.

CThe TSARs are easily characterised and have designed activity allowing
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Paraclesure: Page 36: 255pp: English.

Comprising a binding domain and an effector domain bisclosure: Page 36: 255pp: English.

COV 70470 is a generic DNA Sequence used to generate random TSAR (Totally Syrthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)8(CNB)(NNB)8(CNB)(NNB)8 (CAC)(NNB)8.

CCAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same content of sequences (Q7041-73) have invariant histidine residues content generic sequences (Q7041-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated therefore the peptides or peptides, comprising at least two functional cregions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or compens. comprising a TSAR binding domain can be used in vivo to
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/note= "encoded by Z (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                               defection in a screening process.
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31; Mismatches 77
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Q70470 standard; DNA; 114 BP.
Q70470;
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30-DEC-1993; US-176500,
31-JAN-1994; US-189331,
(UNIC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI: 94-279739/34.
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Terrange proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure, Page 35; 255pp; English.

Disclosure, Page 35; 255pp; English.

CO 70466 is a generic DNA sequence used to generate random TSAR (Totally STATE) and Y are flanking restriction sites (X is not the same as Y)

CC 5yr. X and Y are flanking restriction sites (X is not the same as Y)

CC 70466-68. Other specific peptides generated by these generic sequences

CC repetides, comprising at least two functional regions - a binding of domain with affinity for a ligand and a second effector peptide portion

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deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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WPI; 94-279739/34.
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31-JAN-1994;
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Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins per comprising a binding domain and an effector domain proteins or placing a paneric based to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB) [GGC](NNB) 11Z(NNB) 14(TGC)(NNB) 3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified further or generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-64. TSARs are concatenated by tribey may further comprise a linker chantically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eq. metal ion, and addisocope, peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma denders and therefore circumvent the need for complex methods of hybridoma denders and therefore circumvent the production. The TSARs are easily characterial and have des
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                                                                                                                                                                     domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of 6, 9 or 12 nucleotides (see comments)"
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                                     Length 114;
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/note= "this sequence represents
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Pred. No. 7.85e-04;
29; Mismatches 79;
                                                             No. 5.60e-05;
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4
G;
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55..60
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Q70465 standard; DNA; 114 BP
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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Local Similarity 3.6%;
0 A;
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Best Local Similarity
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direct and rapid detection in a screening process.

US-08-968-800-1.rng

standard; DNA; 114 BP.

7. 13 Q70469

RESULT

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PT Screening a recombinant vector library expressing fusion proteins
PT Screening a Lecombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC spresented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10v. X

CC and Y are flanking restriction sites (X is not the same as Y) that are
CC other specific peptides generated by these generic sequences are shown in CC other specific peptides generated heterofunctional proteins or peptides.

CC other specific peptides generated heterofunctional proteins or peptides.

CC and I least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with the expressed peptide contains or peptide portion that is peptide between the 2 domains. The oligonucleotides are also designed so in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or comprising a TSAR binding domain can be used in vivo to calliver a chemically or biologically active moiety, eg. metal ion, cell: They can also replace the function of macromolecules, eg.

CC deliver a chemically or biologically active moiety, eg. metal ion, cell: They can also replace the function of macromolecules, eg.

CC complex methods of hubridoms function of macromolecules, eg.
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                      /*tag= a
/ncs= "this sequence represents 'Z'; Z can
sequence of 6, 9 or 12 nucleotides (see
comments)
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31-JAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
FOWINES DM, KAY BK;
WPI; 94-2797354.
P-PSDB, R65154.
Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion
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Pred. No. 7.85e-04;
29; Mismatches 79;
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Q70468 standard; DNA; 114 BP.
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Similarity 3.6%;
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Best Local Similarity
Matches 4: Conserv
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01-FEB-1994;
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     070469;
07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library,
TSAR; totally synthetic affilnity reagent; synthetio; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnnnn 60
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
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6.1%; Pred. No. 1.03e-02;
ative 27; Mismatches 80; Indels
                                                                                                                                                                                                              Identifying proteins or peptide(s) which bind a ligand - screening a recombinant vector library expressing fusion
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/note= "this sequence represents '2'; Z
sequence of 6,9 or 12 nucleotides (see
comments)"
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
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05-APR-1995 (first entry)
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Gaps

79; Indels

174 tgtgaatacacacggaagctacaagtgcttttgcctcagtggccacatgctcatgccaga 233 bnabnabnabnabnabnabnabnabnabnabtgcanbnabnabnabnabnabnannnnn 62

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Terbus; Nobles:

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain

Comprising a binding domain and an effector domain

Comprising a binding domain and an effector domain

Comprising at least two functional regions - a binding domain with

Comprising at least two functional regions - a binding domain with

Affinity for a ligand and a second effector peptide portion that is chart the expressed peptide contains 2 or 4 cysteine residues positioned

Comprising at least two functional rigidity to the peptides a linker affinity for a ligand and a second effector peptide portion that is chart the expressed peptide contains 2 or 4 cysteine residues positioned

Comprising the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs

Confer some degree of conformational rigidity to the peptides on the cell-ver a chemically or biologically active modety, eg. metal ion, calivors and also replace the function of macromolecules, eg.

Coll-ver an also replace the function of macromolecules, eg.

Complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP; 0 A; 0 A; 2 C; 2 G; 2 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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29; Mismatches 80; Indels
                                                                                                                                                sequence of 6, 9 or 12 nucleotides (see comments)"
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/note= "encoded by 2"
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ID 070472 standard; DNA; 114 BP.
AC 070472;
DT 10-APR-1995 (first entry)
DE Generic DNA sequence to generat
KW TSAR; totally synthetic affinit
KW direct domain; concatenated h
KW direct; rapid; detection; scree
OS Synthetic.
FF Key
FT misc_feature 55..60
FT //tag= a
FT
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31 - JAN - 1994; US - 189331.
(UYNC - ) UNIV NORTH CAROLINA.
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/note= "this
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3; Conservative
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Matches 3; Conser
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Query Match 8.4%; Score 25; DB 12; Length 114; Best Local Similarity 10.1%; Pred. No. 1.03e-02; Matches 11; Conservative 24; Mismatches 74; Indels 0; (

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Db 66 bunbunbunbunbcacnnbunbunbunbunbcaccacnnbunbunb 114

Search completed: Sat Apr 24 22:27:17 1999 Job time : 66 secs.

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 n.a. database search, using Smith-Waterman algorithm n.a. Psrch_nn

Sat Apr 24 22:17:30 1999;

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MasPar time 484.95 Seconds 1107.807 Million cell updates/sec

Tabular output not generated.

>US-08-968-800-1 (1-300) from US08968800.seq 299 Title:

1 ggctggagaagaaacagcaa.......atagctgtgaagacacagaa 300 ccgacctcttcttgtcgtt.......tatcgacacttctgtgtgtctt Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch 2275026 seqs, 895388244 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-est56 Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est109 Database:

5:9b_est1 6:9b_est10 7:9b_est11 8:9b_est12 9:9b_est13 10:9b_est14 11:9b_est15 12:9b_est16 13:9b_est17 114:9b_est18 15:9b_est2 17:9b_est2 17:9b_est2 18:9b_est2 19:9b_est2 19:9b_est2 19:9b_est2 19:9b_est5 22:9b_est6 23:9b_est7 24:9b_est8 25:9b_est9 26:9b_gss1 27:9b_gss2 28:9b_gss3 29:9b_gss4

Mean 9.757; Variance 1.776; scale 5.495 Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	Result No.	Score	Query	Query Match Length DB	DB	ΩI	Description	Pred. No.
i	-	113		420 18	18	AA913032	ol34a06.sl Soares_NFL_	1.05e-185
υ	7	54	18.1		12	AA754459	97SN1787 Rice Immature	9.83e-62
	m	52	17.4	252	12	AA754459	97SN1787 Rice Immature	8.07e-58
O	4	43	14.4		12	AA754458	97SN1784 Rice Immature	1.16e-40
	2	41	13.7		12	AA754458	97SN1784 Rice Immature	5.67e-37
υ	9	39	13.0	334	10	AA614649	np48a02.s1 NCI_CGAP_Br	2.46e-33
	7	27	0.6		11	AF034173	Homo sapiens ntcon2 co	4.91e-13
	æ	26	8.7		σ	W09270	ma05h07.rl Soares mous	1.68e-11
	6	26	8.7		21	W82677	me98d07.rl Soares mous	1.68e-11
	10	26	8.7		21	AA028399	mille01.rl Soares mous	1.68e-11
	11	26	8.7		7	AA497481	vh29c03.rl Soares mous	1.68e-11
	12	56	8.7		13	AA793395	vn52d12.rl Barstead mo	1.68e-11
O	13	24	8.0		Ξ	AF034173	Homo sapiens ntcon2 co	1.54e-08

/note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as viracer in a subtractive hypridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made

1. .420 /organism="Homo sapiens"

Location/Qualifiers

FEATURES

υ		23	7.7	418	13	AA866946	12d09.rl Strat	4.12e-07
	L T			4 4 4 0 7 4 7	9 T	81. 567	HOMO SA -f-11-0-	4.12e-0/
	17			545	18	. 9	-R-C2p-ng-e-10-0-UI	
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C	40		•	700			6185 Human retina CONA	:-
,	1 (~)			136			yc68q12.s1 Homo sapien	: ':
U	~			310			EST98789 Homo sapiens	٠;
O	010			326			EST02224 Homo sapiens	Τ.
U	. N		•	367			yn48aU4.ri Homo sapien FST32687 Fmbrvo 12 we	
O	10			398			HS_2217_B2_F10_MF CIT	
	7		•	436			mj50g04.rl Soares mous	
	28		0.0	473		W92242	zel4b12.rl Soares feta	2.18e-04
C	7 m			4 / /			cavelus.si homo sapien ot69c07.sl Soares tota	
,	m			547			vx02c07.rl Soares 2NbM	
	32		•	298			HL03789.5prime HL Dros	
	2) C 2) A		•	400		_	Fugu rubripes GSS sequ	
	ე ი ტ. ი			200			MUSSULZ.II SOGIES ZNOM	
	n 19			350			vc45h02.sl Homo sapien	4.24e-03
υ	m			447			vv65h02.rl Stratagene	.24e-0
	m		•	456			yy94c01.s1 Homo sapien	.24e-0
	33			486			yc66c10.s1 Homo sapien	.24e-0
	0.4			514			ᆏ.	\sim
,	4.		•	266		T67696	Homo sapie	.24e-0
J	0 # 7		•	200		C81340	Mus musculus 3.5-apc b	246-0
	C 4 4			744	. r	04034	THED-2325FR TV CI	0 0
J	C 4.4			923	56	AQ253334	6_B1_HO9_MR CIT	.24e-0
						ALIGNMENTS		
,д, ,	RESULT 1							
Н	rocus	AA913	032	42		,	EST	P-1998
u	DEFINITION	ol34a IMAGE	ol34a06.s1 S IMAGE:152533	őo	res_NE 3'sin	T_GBC_S1 ar to SW:	Homo sapiens cDNA clone FBN1_MOUSE Q61554 FIBRILLI	CIN 1
•	MOTOGOOM	אר א היים איני		JIII / /	W.	educince.		•
4 4	MILLESSION	43052	707					
. 34	KEYWORDS) () () () ()	*					
. 0.	SOURCE	human						
•	ORGANISM	Ношо	Homo sapiens	•				
		Eukar		leta2	og.	ordata;	rtebrata; Mammalia;	Eutheria;
•		Primates;		Catarrhini;	hin	; Hominidae;	; Ното.	
-	AUTHORS	NO.		3 2	0 5	chi.n]	h.gov/ncicgap.	
	TITLE	National	nal Car	Cancer Insti	Inst	titute, Cancer	er Genome Anatomy Project	CGAP),
		Tumor	Gene	Index				
	COMMENT	Unpubli	spec	(195	2			
,		Conta	ct: Rol	bert	Str	Contact: Robert Strausberg, Ph.D	D.	
		Tel:	(301)	196-1	550	:		
		Email		ון אַר	raus		· IN II democrate occur	+ +000
		IMAGE		tium Tium	(11		v) for further	
		Insert	t Lengt	ä	169	Length: 1169 Std Error	: 0.00	
		Sed b	orimer:	-40u	113	wd. ET from	Amersham	
	FEATITRES	High		/ sec	luen(ity sequence stop: 68.		

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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnollophyta; Lillopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .252
/organism="Oryza sativa"
/organism="Milyang23"
/note="Vector: piluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3'end with Xho I site."
from the same 3 libraries. The pools consisted of 7.84.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.087.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.287.08-7.28
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Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 252)
Mhm. B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Bun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 GGGACAGTGTCAGCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCCAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 CAAGTGCAAGTGTCATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 TGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 tggaatgaaaccccggccatgccaacacagatgtgtgaatacacacggaagctacaagtg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 CTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 gggagtctgtgaagctacatgcgaacctggatgtaagtttggtgagtgcgtgggaccaaa 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                       Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                          Score 113; DB 18; I
Pred. No. 1.05e-185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Sumon, Kyunggido, Korea
Fel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 CTCCATGGCAAACTGTCAGTATGGCTGTGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poales; Poaceae; Oryza.
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37.8%;
Best Local Similarity 70.7%;
Matches 191; Conservative
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/clone_lib="Rice Immature Seed Lambda 2APII cDNA Library"
/issue_type="Immature Seed"
/dev_stage="5 days after pollination"
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21 c 12 g 35 t 179 others
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Eukaryotes, Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA754459 252 bp mRNA EST 20-JAN-1998
978N1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
cDNa clone 978N1787, mRNA sequence.
AA754459
92801165
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Tel: 82 331 290 0307
Email: myeun@sun2O.asti.re.kr
Submitted by Basek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                   61 SIMIWGIVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRWAHYHDYTNCBBYNNND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     208 ggcaaaagcacttgtagcttccgtgtgtattcacacatctgtgttggcatggccggggtt 149
                                                                                                                                                                                                                                                                                                                                      267 catggcacatgtcctngagttcacacacgtagcatctggcatgagcatgtggc-cactga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YHMWHBBMYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMH 180
                                                                                                                                                                                                                                                                                               1 HWDCTMNIVRGCCCCBAMMIISYBCHGNBVWVCVASHGNYMSVHNCIBRGTHCDCKNVNW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GYWCSBBVKYHIKVSTIRAIRSYICVRKYCVMWMIKKVVKKYHVVBB-GCHBIDSKCKIM 239
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 252;
                                                                                                                                                                                                18.1%; Score 54; DB 12; Length 252
Larity 13.0%; Pred. No. 9.83e-62;
Conservative 121; Mismatches 95; Indels
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
/clone="97SN1787"
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                                                                                                                                                                   Ouery Match
Best Local Similarity 1
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7

82

24

Query Match

Best Loc Matches

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BASE COUNT

ORIGIN

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/crganism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluesript SK(+); Site_1: EcoRI; Site_2:
XhoT; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA754458 247 bp mRNA EST 20-JAN-1998
97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1784, mRNA sequence.
AA754458
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                         260 catgiccingagiticacacacqitagcatiggcatgagcatgiggcc-actgaggcaaaa 202
                                                                                                                                                                                                                                                           HCRYIVBWYYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                AYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 SVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDC 172
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             Gaps
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Pred. No. 5.67e-37;
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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             Mismatches 101;
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             98;
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10.1%;
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ZAPII CDNA Library Oryza sativa
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Embryophyta, Tracheophyta, seed plants, Magnoliophyta, Liliopsida,
Poales, Poaceae, Oryza.
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: M13 Reverse Primer.
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Nahm, B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R. Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 VDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHWWHBBMYBBTGCMTCTMWCWBHYN 146
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                                                                                                                                                                                                                                                                                                                                                                                             27 GNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTK
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                                                                                               179 others
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Pred. No. 8.07e-58;
104; Mismatches 77; Indels
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/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 ot)
days after pollination" coli SOLR" 12 g 35 t 179 ot
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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Pred. No. 1.16e-40;
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97SN1784 Rice Immature Seed Lambda
cDNA clone 97SN1784, mRNA sequence.
4A754458
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/organism="Oryza sativa"
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                                                                                                                                                                                                                                                                    Local Similarity
nes 27; Conserv
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// Organism="Memo sap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                np48a02.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129514, AA614649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 334)
                                                                     173 GGGCWRKVIYGSSBYBRCGVNVMVRTISMWIDKSTKWBSMDMSRRSRVHYGRWMBNKK 230
                                                                                                   144 ITCCIACCTIGATTACAGGITTITCCAGCATAACCAGGATGACACTIGCACTIGITIGGC 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 318.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 10; I
Pred. No. 2.46e-33;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.lln1.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 68.98;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                           human.
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                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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Submitted (13-NOV-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
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1 (bases 1 to 311)

Marra, M., Hillie, I., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Rucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tan, F., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
2275 bp mRNA EST 22-DEC-1997 ntcon2 contig mRNA, partial sequence, mRNA sequence.
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                                                                                                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarnhni; Hominidae; Homo.
1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1476 AAMWRYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYK 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 aacacagatgtgtgaatacacaggaagctacaaagtgctttgcctcagtggccacatgc 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2275;
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Pred. No. 4.91e-13;
50; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map-"optl.3"
/clone-"ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1536 KYTSTYYKSWSRWYWYTTYTYWYCWCCTSMKSAS 1569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="6"
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Local Similarity 10.6%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619 c
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                    Homo sapiens
AF034173
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
Mus musculus
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1 (bases 1 to 473)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Bessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 atgccaacacagatgtgtgaatacacacggaagctacaagtgcttttgcctcagtggc 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AIGCCAGCAAGACIGIGIGAACACGIICGGCAGCIACGAGIGICAGIGCCGCAGIGGC
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="403597"
/clone_lib="Soares mouse p3NMF19.5"
/dev stage="19.5 dec total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 21; Lei
Pred. No. 1.68e-11;
0; Mismatches 16;
   Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 353.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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Best Local Similarity 72.4%;
Matches 42; Conservative
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BASE COUNT
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JOURNAL
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                                                                    FEATURES
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//UDGITIONED MUSCALLA.

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me98d07.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 403597 5'
similar to gb:MZ2488 BONE MORPHOGENETIC PROTEIN 1 PRECURSOR
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Unpublished (1996)
On Sep 13, 1996 this sequence version replaced gi:1393691.
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                             MGI: 200469
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xrer_

/clone="303709"

/clone_lib="Soares mouse p3NMF19.5"

/dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"

/R2 c 88 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 9; Length 311;
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                     quality sequence stop: 290.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                        Seq primer: mob.REGA+ET High quality sequence s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                larity 72.4%;
Conservative
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Best Local Similarity
Matches 42; Conserv
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Gaps

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AA497481 483 bp mRNA EST 01-JUL-1997 vh29c03.rl Scares mouse mammary gland NbMMG Mus musculus cDNA clone 876868 5' similar to SW:BMPl_MOUSE P98063 BONE MORPHOGENETIC PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/65"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 315 26 1800
Final: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="464184"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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Pred. No. 1.68e-11;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 420
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                       137 g
                                                                                                                                                                                                                                                                            /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.4%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                  <1. .>473
a 126 c
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JOURNAL
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KEYWORDS

RESULT

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FEATURES

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r 3']; double-stranded CDNA was lighted to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7r3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library Constructed and normalized by Bento Soares and M.Fatima Bonaldo."
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tan, E., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vn52di2.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone 1024823 5' similar to gb:M22488 BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.
AA793395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                         /clone_lib="Soares mouse mammary gland NbMMG" /sex="male"
                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 7; Length 483;
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 475.
Location/Qualifiers
1. .554
                                                                                                                                                                                                                /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                  100
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                                                                                                                                   /db_xref="taxon:10090"
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                            130 g
                                                                                                                                                         /clone="876868
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.4%;
Matches 42; Conservative
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130 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 418)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:574633
                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"/strain="C57BL/6"
                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 388.
Location/Qualiflers
1. .418
                                                                                                                                                                                        Waterston, R.
                       Mus musculus
  house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA866946 418 bp mRNA EST 16-MAR-1998 vn42d0.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone 1023877 5', mRNA sequence.
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Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens

Eukaryotae, Metazoa: Chordata; Vertebrata; Mammalia; Eutheria;

Primates: Catarrhin1; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis,N. and Ragoussis,J.

Tripodis,N. and Ragoussis,J.

Generation of a transcription map in the region immediately

centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 aaagcatctgcatttgtttggtcccacgcactcaccaaactta-catccaggttcgcatg 38
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myotubes and producing
                                                                                                                                                                                                                                                      Gaps
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                 characteristic muscle proteins."

/db_xxef="faxon:10090"

/clone="1024823"

/clone="1104823"

/celo_lib="Barstead mouse myotubes MPLRB5"

/cell_line="C2C12"

/ cell_line="C2C12"

/ 1155 c 140 g 114 t
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                                                                                                                                                                                                         Length 554;
                                                                                                                                                                                                         Score 26; DB 12; Length 554;
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
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Pred. No. 1.54e-08;
52; Mismatches 29; Indels
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/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
t 619 c 470 g 599 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .2275
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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Best Local Similarity 13.5%;
Matches 13; Conservative
                                                                                                                                                                                                         Query Match 8.7%;
Best Local Similarity 72.4%;
Matches 42; Conservative
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/note="Organ: skin; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5,
adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
/db_xref="taxon:10090"
/clone="1023857"
/clone="lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
human clone=201021 primer=M13RP1 library=Soares fetal liver spleen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R99817 446 bp mRNA EST 14-SEP-1995 yq69b11.rl Homo sapiens cDNA clone 201021 5' similar to SP:FBN1_HUMAN P35555 FIBRILLIN 1;.
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                        295 GACTGCAGGTAATCCCACCGGACCCTGGAAGTCATCTCCATTCATGTGG 343
                                                                                                                                                                                                                                                                                                                                                   Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 13; Length 418
Pred. No. 4.12e-07;
0; Mismatches 13; Indels
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                                                                                                                                                                                                                /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
91 c 116 g 89 t
                                                                                                                                                                                                 /sex="females"
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 73.5%;
Matches 36; Conservative
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Beuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopersygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archonta; Petrapoda; Amniota; Mammalia; Theria; Butheria; Archonta; Petrapoda; Amniota; Mammalia; Theria; Libita; L
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Search completed: Sat Apr 24 22:25:49 1999 Job time: 499 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm n.a. Psrch_nn MasPar time 2494.84 Seconds 1525.983 Million cell updates/sec

not generated. Tabular output

gu ou:

Thu Apr 29 03:05:32 1999;

>US-08-968-800-2 (1-1611) from USO8968800.seq 1607

1 ggctggagaagaaacagcaa......aattactagctgaaaaattg 1611 ccgacctcttctttgtcgtt......ttaatgatcgactttttaac Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap Scoring table:

Dbase 0; Query 0 Nmatch STD 602357 seqs, 1181590623 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl genbank110

16:gp_bal 17:gp_ba2 18:gp_htg 19:gb_in 20:gp_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi

Database:

Mean 11.423; Variance 5.514; scale 2.072 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Re	Result	· ·	Query		å			7
•	. NO.	score	Match	Match Length UB	8	ıυ	Describtion	Fred. NO.
υ	٦	108	6.7	7218	22	I66494	Sequence 14 from paten	1.81e-60
O	7	41	2.6	215	22	128278	Sequence 5 from patent	1.24e-09
	3	37	2.3	2070	19	AF051401	Caenorhabditis elegans	4.99e-07
	4	37	2.3	2139	19	AF051402	Caenorhabditis elegans	4.99e-07
υ	S	37	2.3	10772	13	AF012089	Drosophila melanogaste	4.99e-07
	9	35	2.2	7218	22	I66494	Sequence 14 from paten	9.13e-06
	7	36	2.5	9662	26	HUMFIBRLLN	Homo sapiens fibrillin	2.15e-06
	00	36	2.5	9940	56	HSFIBRMR	H.sapiens mRNA for fib	2.15e-06
	σ	35	2.5	10772	19	AF012089	Drosophila melanogaste	9.13e-06
O	10	36	2.2	74371	27	AC005369	Homo sapiens chromosom	2.15e-06
	11	33	2.1	2156	56	HSFIBUC	H.sapiens mRNA for fib	1.56e-04
	12	33	2.1	2349	26	HSFIBUA	H. sapiens mRNA for fib	1.56e-04
	13	33	2.1	2359	56	001244	Human fibulin-1D mRNA,	1.56e-04

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2525 26 26 2830 29 29 29 29 29 29 29 29 29 29 29 29 29	18 238893 18 HS90L6 Human DNA sequence *** 3.53e- 1548 24 GMNGMIG SOYDER NGMIG Gene Co 1.29e- 17 2823 26 HSFIB5 H.sapiens mRNA for fib 1.29e- 18 3593 19 CELC56E6 Caenorhabditis elegans 4.60e- 17 35593 19 CELC56E6 Caenorhabditis elegans 4.60e- 17 12553 18 AC005513 *** SEQUENCING IN PROG 4.60e- 17 12553 18 HS329A5 Human DNA sequence *** 4.60e- 17 18338 18 HS329A5 Human DNA sequence *** 4.60e- 17 16021 27 HUAC004787 Homo sapiens Chromosom 4.60e-	0 H · · H 0 H 2 L	17218 /organism="unknown 1944 a 1491 c 1486 g imilarity 1.6%; Score imilarity 1.6%; Pred. 6, Conservative 331; M	YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
222222222222222222222222222222222222222	411111111111		194 13mil 6;	rxxxxxxx ccttatgt rxxxxxxxx
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Barth,J.L., Argraves,K.M., Roark,E.F., Little,C.D. and Argraves,W.S.
Isolation of chicken and nematode fibulin-1 homologs and characterization of the nematode fibulin-1 gene
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                           851 ttccctttttacctccatgagagttcccgcctctggaaactatcttcatagttgaag 792
                                                                                                  731 titgccttcttttttcatgctgtttttgtgagcaagcaacttcttgattctgtttgatg 672
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to
control fungal disease
Patent: US 5569830-A 5 29-007-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 tatactgacagtttatcatggca-catgtcctngagttcacacacgtagcatctggcatg 225
                                                                                                                                                                                                                                  30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 ccaggoggagtcctgaggatggacacaggcactgtgggccttcttctgtgtcttcacagc 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 NYGGNNVGAAKTHYYTHINVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SSSSVVSRTASCNDKAKKDGNTISSWITDCCNRTWGVCDTDTIYRVNNDSGHNKYSSANY 66
                                                      791 ggctgcaagttcaccttaggggtaggagtcctggtgggttctgggggtaacatttttaatt
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Pred. No. 1.24e-09;
82; Mismatches 91; Indels
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Sequence 5 from patent US 5569830.
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Best Local Similarity 16.3%;
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SSHCEHLCHORGGEKVECSCRSGFDLAPDGMACVDIDECATLMDCLESGRCLNFPGS
FRCIRTLSCGTGYAMDSETERRADDECNLGSHDCGPLYCRNTGGSTRCDARKCGDG
ELONPMIGECTSITCPNGTYPRNGMCNDIDECVTGHNCGAGEECVNTPGSFRCODKS
LCAHGYEVNGTGFCEDVNECOOGVCGSMECINLPGTYRCKCGPGYEFNDAKKRCEDV
VNIPGSYQCICDRGFALGPDGTRCEDIDECSTWAGSGNDLCMGGCINTRGSYLCOCPP
GYRIQPDGRTCVDVDECAMGECAGSDKVCVNTLGSFRCHSIDCPTWTHROSYLCOCPP
DGYSCIRVCSTEDFECLGNHTREVLYQFRAVPSLKTIISPIEVSRIVTHMGVPFSVDIA
NLDYVGQRHFRIVOERNIGIVQLVKFISGPTVETISTISTISTISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="fibulin-1 isoform D precursor"
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DLLNNREPCVAPVGFSAGCLRSFNKCCNGDIEITHASEIITGRPLNDPHVLHGGBRCA
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Barth, J. L., Argraves, K. M., Roark, E. F., Little, C. D. and Argraves, W. S.

Isolation of chicken and nematode fibulin-1 homologs and characterization of the nematode fibulin-1 gene
                                                                                                                                                                                                                                                                                                  /map="between elt-1 and daf-10"
/note="partial sequence obtained from EST clone ykllbl"
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precursor (FBLN1) mRNA,
                                                                                                                                                S_{C}
2 (bases 1 to 2070)
Barth,J.L., Argraves,K.M., Roark,E.F., Little,C.D. and Argraves,W.S.
Direct Submission
Submitted (26-FEB-1998) Cell Biology and Anatomy, Medical
University of South Carolina, 171 Ashley Avenue, Charleston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 ICTGGATTCGACTTGGCACCAGATGGAATGGCTTGTGTAGATATTGATGAGTGTGCCACA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 4.99e-07;
0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="extracellular matrix protein"
                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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BCCIKRAGHVCDLSAECINTIGSFECKREPGPLASDGKRCEDVNECTTGIACEDV
VNI PGSYQCICUPGFALGPDGTKCEDIDECSIWAGSGNDLCWGCINTKGTTGCCOP
GYKIQPSQCICUPGFALGPDGTKCEDIDECSIWAGSGNDLCWGCINTKGSLNCCOP
GYKIQPSGTCVDDVBCAMGECAGSDKVCVNTLGSFKCHSIDCPTNIHDSLNKNRCN
RQPSACGLPEECSKVPLFLTYQFISIARAVPISSHRRAITLFKVSAPNHADTEVNFEL
QLKTIVGAPBVLPAIRANTVHPPLMKIRN
NFNYZAANLIVDVAAHRRHNTVHPPLMKIRN
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SSHCEHLCHDBGGEKVECKRGFDLAPDGMACVDIDECATLMDDCLESORCLNTPGS
FKCIRTLSCCTGYAMDSEIERRENDVDCNLGSHDCGPLYQCRNYGGSYRCDAKKGDG
ELQNPWTGECTSITCPNGYTPRNGMCNDIDECVTGHNCGAGEECVNTPGSFRCQDKG
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\[ \frac{1}{0} \text{xref} = \frac{1}{0} \text{sref} =
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P-element-induced recombination in Drosophila melanogaster: hybrid
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                                                                                                                                                                                                                                                                                                                                                                             /map="between elt-1 and daf-10"
/note="partial sequence obtained from EST clone ykllb1"
                                                        Direct Submission
Submitted (26-FEB-1998) Cell Biology and Anatomy, Medical
University of South Carolina, 171 Ashley Avenue, Charleston, SC
29401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAIGGACGAITGITIGGAAICICAACGAIGITIGAAIACICCIGGAAGCITIAAAIGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 TCTGGATTCGACTTGGCACCAGATGGAATGGCTTGTGTAGATATTGATGAGTGTGCCACA 603
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 4553)
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Barth, J.L., Argraves, K.M., Roark, E.F., Little, C.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="extracellular matrix protein"
                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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                                       Argraves, W.S.
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/product="cysteine proteinase-1"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/translation="MRTAVLLPLIALIAVQAVSFADVVMEEMHTFKLEHRKNVQDET
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QLRAADESFKGYTFSSAHVTLPKSVDWRTKGAVTAVKDQGHGGSCWAFSSTGALEGY
HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
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EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
ASSYPLV"
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/db_xref="PID:92305222"
/translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
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SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
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PVVTVQQNFDNLLI PADHVSRQKSDCYY INQOHLLRAHTTAHQVELISGGLDNFLVVG
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                                                                                                                                                                                         University
                                                                                                                      3 (bases 1 to 10772)
Gray, Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, Universi
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
uray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
Onpublished
                                                                                                                                                                                                                                                              Length 10772;
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join(8110. .9300,9370. .>9532)
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Pred. No. 4.99e-07;
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                                                                                                                                                                                                                                                                                                                                                                    /product="cysteine protease"
872. .7707
/gene="CP1"
872. .1000
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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                                   | 1510 atggtactatctttatatttgactttgtatgtcagttccctggttttttgatattgcat 1569
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9662)
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 570367-A 14 23.SEP-1997;
Location/Qualifiers
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    Mismatches 46;
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Hum. Mol. Genet. 2, 961-968 (1993)
93372860
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Pred. No. 9.13e-06; 83; Mismatches 54
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                                                                                                                                                                                 Sequence 14 from patent US 5670367.
166494
92724471
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/db_xref="taxon:9606"
1. .133
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1491 c 1486 q.
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AUTHORS
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WYIPGRPEYPPPLGPIPGYIPWOCCCDAGREWSPOWTAPERDEPTRATEDEPRILEGSYP
DYCQLVRYLCONGRCIPTPGSYRCECNKGFQLINGECINVDGEGRINPOGGETIVRO
GSYTCOCRAGIOSTITRTECRDIDECLOMGRICINNDGERINPCAGGETIVRO
GSYTCOCRAGIOSTITRTECRDIDECLOMGRICINNDGERINPCAGGETIVRO
GRYCCEDAIDECSTRINGLAGGAGITATRECRDIDECLOMGRICINNDGERINPCAGGETIVRO
GRYCCHNIDGSYRCECFGLAVGLDGRVCVDTHMRSTCYGGYKRGOTIRPEGFYTRO
CCCASTERYAFGEPCOPCPAGNISAEYOALCSSEPHIDPTATICIETIKGTCWOT
KRDLKTCEDIDECESSPCINGVCKNSPGSFICECSSESTLDPTKTICIETIKGTCWOT
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VIDGRCEININGATIKROCCSSLGAAMGSPCTLCONPOICGKGYSRIKGTOCEDIDEC
EVFBYCKKNGLCVNTRGSFKCOPFSGMTLDATGRICLDINGETYROEDETILIA
BCKMIPSACCCSSGRAMMKNCMDIDECORPPLLCRGGYCHRTEGSYRCEPPROPI
EVRIPSACKNATGSFKCROSGFALDSEERNTTDIDECRISPDLCGRGQCV
SPNISACIDINCELSAHLGSPKCROSGFALDSEERNTTDIDECRISPDLCGRGQCV
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SPNISACIDINCELSAHLGSRKCROSGFALDSEERNTTDIDECRIPURGSYRCEPPROPI
NGGGEFFTONSGSYRECCPORTANDIDECGNEPPLLCRGGCCHNTRGSFKCRTGC
CLCOGFRASSDMKTCVDVNECDLINNICGRGGCTNIPGESIN
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CLCOGGKCINTPGSFTCSTTDLDECSENINLCGGGGCTNIPGCSING
TGGNGYREAGAGCCSCSGGGGGGFRPNPTINCSCNIC
TGISONCWPRGSYTCCEPPERDELYCTOYLLINEDTROCKOCSINIG
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RAWNRRCEQCEIPSTORGETCTOLDECSONPYCOGRACITYAGSTROCKETYRE
GELGCCGCCACKRAWGTPCCCTOYLLYGFKTNDDGTMCLDINGSTROTY
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RAWNSTROTORGCTORGETCOTORGETCOTORGCTOTORGSTROTY
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/translation="MRRGRLLEIALGFTVLLASYTSHGADANLEAGNVKETRASRAKR
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HRLNEVSQKCEDIDECSTIPGICEGGECTNIVSSYFCKCPPGFYTSPDGTRCIDYRPG
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EPDVCKHGQCINTDGSYRCECPFGYTLAGNECVDTDECSYGNPCGNGTCKNVIGGFEC
TCEEGFEPGPMYTCEDINECAQNPLLCAFRCVNTYGSYECKCPVGYVLREDRRMCKDE
DECEEGKHDCTEKQMECKNLIGTYMCICGPGYQRRPDGEGCVDENECQTKPGICENGR
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RSCKDLDECATKOHNCOFLCVNTIGGFTCKCPPGFTQHHTSCIDNNECTSDINLCGSK
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Pred. No. 2.15e-06;
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/standard_name="Marfan syndrome gene"
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llarity 66.4%;
Conservative
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Best Local Similarity
Matches 73; Conser
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Score 36; DB 26;
Pred. No. 2.15e-06;
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Location/Qualifiers
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9741
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Similarity 66.4%;
73; Conservative
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9898. .990
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Best Local Similarity
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EPSSGCSGHDWEQPPPPPRESEPPLLHWQGPPEVGAAPGEGGRSPARGTGGGTAGPRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-DEC-1991) C.L. Maslen, Oregon Health Sciences Univ, Dept of Mol and Medical Genetics, 3181 S W Sam Jackson Pk Rd, Portland Oregon 97201, USA
3 (bases 1 to 9940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakai,L.Y.
Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' Genomics 17 (2), 476-484 (1993)
                             17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                       Partial sequence of a candidate gene for the Marfan syndrome Nature 352 (6333), 334-337 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corson, G.M., Chalberg, S.C., Dietz, H.C., Charbonneau, N.L. and
                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NGOCINTYGSFOCCOUNGY EVAPDGRICOD INECLLEPRKCAPGTCQNLDGSYRCICP PGYSLONEKCEDIDECVEEPEICALGTCSNTEGSFKCLCPEGFSLSSSGRRCQDLRMS YCYAKPEGGKCSSPKSRNHSKQECCCALKGEGWGDPCELCPTEPDEAFRQICPYGSGI TYGPDDSAVDWDECKEPPVCKHQQCITYDGSYRCECPFGYTLAGNECVDTDECSYGNP CGNGTCKNVIGGFETCEEGFEPGPMYTTGDINECAPRICAFRCWTYGSYEKCC VGYVLREDRRAMCKDEDECEEGFHDCTEKQMECKNLIGTYMCIGGPGYQRRPDGEGCUD EPPVSGEMDDNSLSPEACYECKINGYPKRGRKRRSTNETDASNIEDQSETEANVSLAS WDVEKTAIFAFNISHVSNKVRILELLPALTTLTNHNRYLIESGNEDGFFKINQKEGIS YLHFTKKKPVAGTYSLQISSTPLYKKKELNQLEDKYDKDYLSGELGDNLKMKIQVLLH AF012089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089 92305220 Drosophila melanogaster
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 453)
Gray, Y. H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Direct Submission
Submitsed (30-UNN-1997) School of Biological Sciences, University
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia ö 4482 GATCTGGACGAATGTTCCAATGGAACCCATATGTGCGGCCAGCATGCAGACTGCAAGAAT 4541 502 gatataaatgaatgtactatggatagccatacgtgcagccaccatgccaattgcttcaat 561 Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects Gaps ö 4542 ACCATGGGATCTTACCGCTGTCTGTGCAAGGAAGGATACACAGGTGATGG 4591 /note="either G or T in various cDNA clones" /note="either C or T in various cDNA clones" Length 9940; 2 others 0; Mismatches 37; Indels

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DNA PRI 01-AUG-1998
5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7431)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pilluck,S., Pollard,M., Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                    Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  % (bases 1 to 74371)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Bavis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Sequence submitted by:
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2795_ 2438
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2818_ 2859
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                                                                                                                                                                                                                                                                                                                          /product="cysteine proteinase-1"
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/tanslation="MTRAVLDPLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
EERFRAKITAKHYORPAEGKVSFRLAVNKYADLLHHEFROLMNGFWYTLHK
OLRAADESFKGVTFISPAHVTLEPKSVDWRTKGAVTANKYDGHGGSGARESGTGEG
HFRKSGYLVSLEEDQNLVDCSFRYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEALD
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAYATVGFVSVALDASHESFQFYSEGLYN
EPQCDAONLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
ASSYPLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="phenylalanyl trna synthetase"
/db_xref="plb:g2305222"
/db_xref="PlD:g2305222"
/translation="MiltiryOgarhylkstrclassaaPaksPsSPPOlevsGSTYA
TDGWTNVTPKILSYVGANKHLQTDHPLSIIRORIVNTFYGARNQFREFSYYDOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVYTVQONEDNILLIPADHVSRQKSDCYYINOOHLIRAHTTAHOVELISGGLDNFLVVG
SVYRRDBISTHYPVFHQADAVRLYTKDKLFERNPGLELFESTWSGTLADPKLILPHP
SSWTKPNSPATRAVKLAHERKHVLVOCHTKDLFOFRIKYWTDYFFPTOPSWELET
YFKDNWLEVLGCGINTHEILORISGYHOSIGTARGYGLERLAWVLFDIPDIRLFWNDS
GFLSOFSEKDLHNLPRYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVAG
DMVEQISLVDKFKHPRTGKSSVCFRIVYRHMERTLICQAEVNEIHKQIASASVDSFNVQ
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                               oin(872. .1000,2310. .2426,6476. .6690,6751. .7707)
gene="Cp1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1752 WWAYAWWKMWYRTWARMAMASWARWKWKTSAAAAYSAWRKMWKWWAYRAWKKTWWWAAW 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: : | ::: :: | : |::| :| :| :| : :: | | :: : : | | 433 ggaagctactgcaatgtcacattggtttcgaactgcaatatcagtggacgatat 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4546. .4553
/gene="CP1"
/note="insertion site of P{CaSpeR}(50C)"
/citation=[1]
6476. .6690
/gene="CP1"
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Pred. No. 9.13e-06;
62; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="phenylalanyl tRNA synthetase"
join(8110 .9300,9370 .>9532)
/note="potential orf"
Organism="Drosophila melanogaster"
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                                                                          /product="cysteine protease"
872. .7707
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                    /db_xref="taxon:7227
join(872. .1000,2310
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                                                                                                                                                                      /gene="CP1"
2310.
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872. .1000
/gene="CP1"
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/gene="CP1"
6751. .7707
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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Best Local Similarity 15.5%;
Matches 20; Conservative
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/rpt_family="Alu"

/rote="100% identity EST ou55c09.x1"
/db_rate="3722
/note="100% identity EST ou55c09.x1"
/db_rate="405ST:A1025011"
36901. 37164
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complement(37595. 37654)
/note="GRAIL 2 excellent exon, frame 0"
complement(1010,18063. 38618,38462. 38578,38741. 38995,3901. 39205,39532. 39630,39935. 40048,40300. 40410,40503. 40661,41868. 41972,42103. 42255,42492. 42569,44379. 44507)) ä Db 15931 SRSKSKRGWGYRSWKKYRCAMWMTCKSSKCWCWSYRMRMKCYSCSYCYCSSGKKYWCRCS 15990 Score 36; DB 27; Length 74371; Pred. No. 2.15e-06; 55; Mismatches 29; Indels 1; Gaps /standard_lame="histidyl-tRNA synthetase"
/note="78%-100% protein identity GenPept:U18937"
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complement(30401. 30536)
/note="GRALL 2 excellent exon, frame;
complement(30682. 30733) note-"GRAIL 2 excellent exon, frame frame Db 15991 MYWYTCYYSYKYYWSMSYCTCTSWGWRWMWSKGRSWMYASR 16031 /rpt_family="MLT1"
complement(33670 .33785)
/rpt_family="Alu"
complement(34021 .34144)
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27774. .28057
/rpt_family="Alu"
28040. .28066
/note="(A)27" 'rpt_family="MLT1" 12617. .32908 /rpt_family="Alu" 32977. 32977. Note: remainder of annotations omitted. /rpt_family="Alu" 27191. .27477 Query Match 2.2%; Best Local Similarity 15.8%; Matches 16; Conservative repeat_region misc_feature SIS

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Homo sapiens
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ATEYRRCCHCCLLGRAAQAGGSCEYSLMYGYQCGOVFRACCYKSOBTGDLYYGGLOE
TDK I IEVEEEGEDPYLINDRCRGGGPCKOOCRDTGDEYVCSCFYGYDLLSDGYSCEDYN
EICHTGSHSCRLGESCINTYGSFRCORDSSGGTGYELTEDNSCKDIDGESGTHNOLPD
EICHTGSFRCRPKLQCKSGFIQDALGONDIDINGCLSTSAPCPIGHTCINTGESYTC
FICONTLGSFRCRPKLQCKSGFIQDALGONDIDINGCLSTSAPCPIGHTCINTGESYTC
FICONTLGSFRCRPKLQCKSGFIQDALGONDIDINGCLSSPC
GKRUYDVNECQRYPHLEEGTRCVDVDECAPPAEPCGKGHRCVNSPGSFRCECKTGYYFD
SRWCVDVNECQRYPGRACCHKCENTCSTLCSTSCTINTGSSPC
GPSCANYYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGHICSYRCINTGSFPC
CPSSGYRLAPNGRNCODIDECVTGINGCSINTTCRNIQGAFRCLAFECPERYRRSAAT
RCERLPCHERRESCRLPARTYYHLSFPTNIQAPAVVFRNGPSSAVPGDSMQLAITGG
                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 2156)

Korenberg, J.R., Chen, X.N., Tran, H. and Argraves, W.S.

Localization of the human gene for fibulin-1 (FBLN1) to chromosome
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                                                                                                                                                                                                                    Direct Submission
Submitted (03-JUL-1990) Argraves W.S., American Red Cross, 15601
Crabbs Branch Way, Rockville, MD 20855, USA
2 (bases 1 to 2156)
Argraves,W.S., Tran,H., Burgess,W.H. and Dickerson,K.
Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure
J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
                                               21-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1526 CAGIGCAGCIGCCCCCCGTCIGGCIACAGGCIGGCCCCCAAIGGCCGCAACIGCCAAGAC 1585
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2156)
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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Cytogenet. Cell Genet. 68 (3-4), 192-193 (1995)
95145011
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/product="fibulin-1 C"
/db_xref="PID:g31419"
/db_xref="SWISS-PROT:p23144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
1. .2156
/organism="Homo sapiens"
/db_xref="taxon:9606"
                             H.Sapiens mRNA for fibulin-1 C. X53743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="fibulin-1 C"
2156
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Best Local Similarity 66.3%;
Matches 67; Conservative
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11. .2062
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/translation-"MERAAPSRRVPLFLLLGGLALLAAGVDADVLLEACCADGHRMA
THORDCSLPYATESKECRMVOBOCCHSQLEELHCATGISLANEQDRCATPHGDNASLE
ATFVRCCHCCLLGRAAAGGGSCESTANOTYOCGOVFRACOVKSOETGLLDVGGLQE
TDKIIEWTEBEQEDPTJUNDRCRGGPCRQCOFOTGDEVCSCFVGYQLLSDGVSCEDVN
ECITOSHSCRLGESCINTVGSFRQRDSSCGTGYELTEDNSCRDIDECESGIHNCLPD
FICONTLGSFRCRPKLOCKSGFIQDALGNCIDINECLSISAPCPIGHTCINTEGSYTC
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ISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLSVDGRSCEDINECSSSSPC
SQECANVYGSYQCYCRRGXQLSDVDGVTCEDIDECALPTGGHICSYRCINIPGSFOCS
CPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGAFRCLAFECPENYRRSAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 2349)
Norenbergy, R., Chen, X.N., Tran, H. and Argraves, W.S.
Localization of the human gene for fibulin-1 (FBLN1) to chromosome
band 22q13.3
                                                                                                                                                                                                                                       Argraves, W.S.

Argraves, W.S.

Submitted (103-JUL-1990) Argraves W.S., American Red Cross, 15601

Crabbs Branch Way, Rockville, MD 20855, USA

2 (bases 1 to 2349)

Argraves, W.S., Tran, H., Burgess, W.H. and Dickerson, K.

Fibulin is an extracellular matrix and plasma glycoprotein with J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2349)
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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H.sapiens mRNA for fibulin-1 A.
X53741
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/evidence=experimental
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/product="fibulin-1 A"
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11. .1711
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/codon_start=1
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2 (bases 1 to 9830)
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Best Local Similarity 66.3%;
Matches 67; Conservative
                                  (bases 1 to 2525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /piccef="PID:g1621019"
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ECITGSHSCRLGESCINTVGSFRCQRDSSCGTGYELTEDNSCKDIDECESGIHNCLPD
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LQQEKTDTVRCIKSCRPNDVTCVFDPVHTISHTVISLPTFREFTRPEEIIFLRAITPP
HPASQANIIFDITEGNLRDSFDIIKRYMDGMTVGVVRQVRPYRPVGPFHAVLKLEMNYVV
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2 (bases 1 to 2525)
Argraves,W.S., Tran,H., Burgess,W.H. and Dickerson,K.
Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure
                                                                                                                                                                                                                                                         Direct Submission
Submitted (10-SEP-1993) S. Argraves, Biochemistry, American Red
Cross, 15601 Crabbs Branch Way, Rockville MD 20855 USA
Location/Qualifiers
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2525)
                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A novel form of fibulin produced by alternative splicing
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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Human fibulin-1D mRNA, complete cds.
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/db_xref="taxon:9606"
111. .2122
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H.saplens mRNA for fibulin-1 B.
X53742
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Best Local Similarity 66.3%;
Matches 67; Conservative
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                                                                                             Homo sapiens
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TDKIIEVEEEQEDPYLNDRCRGGPCKQQCRDTGDEVVCSCFVGYQLLSDGVSCEDVN
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FICONTLGSFRCRPKLDCKSGFIQDALGNCIDINECLSISPOPLIGHTCINTEGSSYC
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ISRMCYDVRECQRYFDGRLCGHKCENTLGSYLCSCSVGFRLSVDGRSCEDINECSSSPC
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CPSSGYRLAPNGRNCQDIDECVTGINUCSINETCFNIQGAFRCLAFECPENYRRSAAT
                                                                                             Korenberg, J.R., Chen, X.N., Tran, H. and Argraves, W.S.
Localization of the human gene for fibulin-1 (FBLNI) to chromosome and 22q13.3
Cytogenet. Cell Genet. 68 (3-4), 192-193 (1995)
95145011
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 9830)
Ota,K., Kumar,A., Wada,J., Liu,Z. and Kanwar,Y.S.
Molecular cloning of mouse fibrillin-1 and its role in the renal
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Mus musculus fibrilin-1 (Fbn1) mRNA, complete cds.
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9726323
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
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                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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1. .2525
/evidence=experimental
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                                                                                                                                                                             /product-"fibrillin-1"
     Socation/Qualifiers
1. .9830
                                                                                               /dev_stage="newborn
                                              strain="CD-1"
                                                                                                                         'gene-"Fbn1"
                                                                                                                                     220. .8841
/gene="Fbn1"
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FEATURES
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0; Gaps Query Match 2.0%; Score 32; DB 29; Length 9830; Best Local Similarity 63.8%; Pred. No. 6.25e-04; Matches 74; Conservative 0; Mismatches 42; Indels

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VAPNRCACTYGFTGPQCERDYRTGPCTTVVSNQMCQGQLSGIVCTKTLCCATVGRAWG
HPCEMCPAQPHPCRRGFIPNIRTGACQDVDECQAIPGMCQGGNGINTVGSFECKCPAG
HKFNEVSQKCEDIDECSTIPGYVCDGGECTNIVSSYFCKCPPGFYTSPDGTRCVDVRPG
YCYTALANGRCSNQLPQSITKMQCCCDLGRCWSPGYTVAPEMCPIRSTEDFRKILCSVP LVIPGRPEYPPPPIGPLPPVQPVPPGYPPGYPVIPVPRPPEYPYPSPSREPPRVLPFN ECTCEBGFEPCPMMCEDINECAQNPLLCAFRCVNTYGSTECKCPVGTVLREDRRWCK
DEDECAEGKHDCTEKQMECKNLIGTYMCICGFSTQRRFDGECLIDENECGTRGTCEN
GRCLMTLGSTTCECNDGFTASPTQDECLDNREGYCFSEVLQNMQQIGSSNRNPTKSE
CCCDGGRGWGPHCEICPFEGTVAYKKLCPHGRGFMTNGADIDECKVIHDVCRNGECVN DGRSCKDLDECATKQHNQFLCVNT IGGFTCKCPPGFTQHHTACIDNNECTSDINLCG
SKGVCQNTPGSFTCECQRGFSLDOSGASCEDVDECEGNHRCQHGCQNI IGGYRCSCPQ
GYLQHYQWNQCVDENECLSAHVCGGASCHNTLGSYRCMCPTGFQYEGFSGGCQDINEC
GSQAPCSYGCSNTEGGYLCGCPPGYFRIGQGHCVSGMGMGRGGPPPASSEMDNSL
SPEACTECK INGYPKRGRKRRSTNETDASDIOGSEMEANVSLASWDVSK
SHVNNKYRILELLIPALITLANHNRYLIESGNEDGFFKINQKEGYSYLHFTRKKRVAGT DRGSYHCICKTGYTPDITGTACVDLNECNQAPKPCNFICKNTEGSYQCSCPKGYILQE YSLOISSTPLYKKKELNQLEDRYDKDYLSGELGDNLKMKIQILLH 2371 c 2665 g 2292 t 2502

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Search completed: Thu Apr 29 03:47:27 1999 Job time : 2515 secs.

4306 TGCACAGATCTGGATGAATGCTCTAATGGAACCCACATGTGCAGCCAACACGGGGACTGC 4365

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Query Match 2.6%;
Best Local Similarity 16.4%;
Matches 10; Conservative
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827.661 Million cell updates/sec
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7.10e-11
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ccgacctcttcttgtcgtt......ttaatgatcgacttttaac
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                                                                                                             Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mean 9.403; Variance 5.340; scale 1.761
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1607
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Generic DNA sequence Generic DNA sequence Generic DNA sequence Generic DNA sequence Human endothalin-1 an Generic DNA sequence Human endothalin ETA DNA encoding cell pro Generic DNA sequence	Human interleukin 8 a Sequence encoding thr Sequence encoding thr Sequence encoding thr CDNA encoding human r Encodes truncated human Encodes thrombomoduli Soluble thrombomoduli Soluble thrombomoduli Recombinant thrombomodulin Recombinant thrombomodulin Human thrombomodulin Human thrombomodulin EcoRI fragment encodil	ia; disease diagnosis;	for Mycobacteria - used octeria nucleic acid in sof nucleotides 5-95 of of mycobacteria tested, ial spp. The probe may cobacterial infection.
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0046 0046 0046 0046 0046 0046 0046 0046	17.6363 0005948 0005946 0005946 0005946 010495 010435 010435 010435 010435 010435 010435 010435 010435 010435 010435 010435 010435	ALIGNMENTS P. A mycobacteri	ecifi Mycc Mycc nsis nsis bact for 7 C;
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Score 41; DB 9; Length 91; Pred. No. 2.86e-10; 41; Mismatches 10; Indels

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Fibulin G Fibulin F Fibulin E Generic I

011010 011008 011009 070465

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11 T;

17 G;

47 C;

21 A;

204 BP;

Sequence

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PART-1988; 105163.

PR 30-MAR-1988; 105163.

R 03-APR-1989; 105087.

PR 30-MAR-1988; 105163.

PR 53-APR-1988; 105163.

PR 53-APR-1988; 105163.

PA (SUSO) SUOMEN SOKERI OY.

Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;

PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;

PI Introducing random point mutations into nucleic acods -

PI Introducing random point mutations were introduced into the alpha fragment of malanicorporation, completion of molecules and screening.

PR Random point mutations were introduced into the alpha fragment of c. E. coli beta-galactosidase. The wild type sequence was obtained as a c. c. it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The reserverse transcriptase and the molecules are completed to forms that can be camplified and then expressed in a suitable host-vector system.

C See also P80575.
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
(051735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
See also 051735-45 and 051747-59.
Sequence 91 Bp; 5 A; 17 C; 15 G; 4 T;
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            war ully unuleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in samples
                                                                                                                                                      Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
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No. 2.86e-10;
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                                                                                                                                                                                                                                            EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                         31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
                            Q51746 standard; cDNA; 91 BP. Q51746;
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Programmer of the properties o
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                                                                                                                                                                                                                                                           1325 ttctcccatgccagggcattgttactgttttcacaaacactcgaagtttcccgacttg 1266
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070467 standard; DNA; 114 BP.
070467 standard; DNA; 114 BP.
070467 standard; DNA; 114 BP.
050467 standard; first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker;
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108 Others;
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N81164;
08-NOY-1990 (first entry)
E.coli beta galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment.
Escherichia coli.
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                                                         Score 42; DB 1; Length 204;
Pred. No. 7.10e-11;
51; Mismatches 33; Indels
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Pred. No. 2.86e-10;
57; Mismatches 42; Indels
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187..204
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Matches 10; Conservative
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31-JAN-1994;
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                                                                                                                 Fowlkes DM,
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P-PSDB;
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                                                                                                                                                                                                                                              Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain placing a binding domain and an effector domain bisclosure; Page 35, 255pp; English.

O70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)12. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides. Comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains The oligonucleotides are also designed so
                                                                                                                                                                                                                                                                                                                                                                                                                                                           that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compress. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
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Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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  detection; screening; treatment; generic; ss
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Pred. No. 3.70e-06;
33; Mismatches 71; Indels
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/note= "this sequence represents '2'; 2 s
sequence of 6, 9 or 12 nucleotides (see
                                                                      s sequence represents 'Z'; Z
6, 9 or 12 nucleotides (see
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sequence of 6,
comments)"
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Q70468 standard; DNA; 114 ВР.
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Similarity 1.9%;
2; Conservative
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US-176500.
US-189331.
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direct; rapid;
Synthetic.
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31-JAN-1994;
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production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Pred. No. 3.70e-06;
33; Mismatches 75; Indels
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                                                                                                           NORTH CAROLINA Kay BK;
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Similarity 3.6%;
4; Conservative
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US-176500.
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Best Local Similarity
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070469;
070469;
07-687-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be
sequence of 6,9 or 12 nucleotides (see
comments)"
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Pred. No. 3.70e-06;
33; Mismatches 75; Indels
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UNIV NORTH CAROLINA.
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Best Local Similarity 3.6%;
Matches 4; Conservative
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
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CC (70469 is a generic DNA sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TGC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
csites (X is not the same as Y) that are cloverleaf in structure. Other
CC generic sequences are shown in 070465-68. Other specific peptides
CC generic sequences are shown in R65150-54. TSARS are
CC concatenated beterofunctional proteins or peptides, comprising a least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
CC a second effector are also designed so that the expressed peptide
active. They may further comprise a linker peptide between the 2 domains.
CC ortains 2 or 4 cysteine residues positioned in, or flanking, the
CC onformational rigidity to the peptides. The TSARS or compose. Comprising
CC offormational rigidity to the peptides. The TSARS or compose.
CC offormational rigidity to the peptides. The TSARS or compose.
CC offormation of macromolecules, eg. menoclohal or polyclohal antibodies
CC of enzyme, to the specific target or on the cell. They can also replace
CC offormation of macromolecules, eg. menoclohal or polyclohal antibodies
CC formation or in vivo antibody production. The TSARS are easily
CC characterised and have designed activity allowing direct and rapid
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Claim 10; Fig 3; 56pp; English.

The fibulin C cDNA was sequenced from a clone isolated from lambda git1 human placental cDNA library using a polyclonal antiserum.

The three forms (A, B and C) are identical from their 5, ends to a divergence point at posn. 1707, after which they are distinct through to the poly(A) tail. The cDNA can be used to express
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/label= point of divergence
2126.2131
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98..2059
/*tag= b
/product= fibulin C
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Q11010 standard; cDNA; 2200 BP.
Q11010;
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6; Conservative
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Fibulin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LJOL-) LA JOLLA CANCER REG
(AMNA-) AMER NAT RED CROSS.
Ruoslahti El, Argraves WS;
WPI; 91-087250/12.
N-PSDB; R11150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1989; US-395773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-1990; U04662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 cagtgcctgtgtccatcctcaggactccgcctggccccaaatggaagagactgtctagat 369
                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Claim 10; Fig 3; Spp; English.

The fibulin A cDNA was sequenced from a clone isolated from lambda gt11 human placental cDNA library using a polychonal antiserum.

The three forms (A, B and C) are identical from their 5' ends to a divergence point at posn. 1707, after which they are distinct through to the poly(A) tail. The cDNA can be used to express recombinant fibulin in a host cell. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion be used to manipulate adhesion of cells to fibronectin, collagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 91-087250/12.
N-PSDB; R11148.
Purified fibulin, DNA encoding it and antibodies reactive with it
recombinant fibulin in a host cell. Fibulin binds to the vytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDRA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen,
                                                                                                                        laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also 011008 and 011009.

Sequence 2200 BP; 464 A; 654 C; 647 G; 435 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also 011009 and 011010.
Sequence 2355 BP: 526 A; 668 C; 682 G; 479 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                Length 2200;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches 34; Indels
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larity 66.3%; Pred. No. 1.36e-05;
Conservative 0; Mismatches 34
                                                                                                                                                                                                                                                                                Score 33; DB 2; I
Pred. No. 1.36e-05;
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/label= point of divergence
2286..2291
/*tag= d
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98..1708
/*tag= b
/product= fibulin A
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Q11008,
21-MAY-1991 (first entry)
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(LJOL-) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
                                                                                                                                                                                                                                                                                2.1%;
Local Similarity 66.3%;
les 67; Conservative
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07-MAR-1991, 004662, 17-AUG-1990; US-395773, 0.0
0.094, 0.084, 0.08773, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.0878, 0.
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- useful as diagnostic and therapeutic component.

Claim 10; Fig 4; 56pp; English.

Claim 10; Fig 4; 56pp; English.

The fibulin B CDNA was sequenced from a clone isolated from lambda gill human placental CDNA library using a polyclonal antiserum.

The three forms (A, B and C) are identical from their 5' ends to a divergence point at poss. 1707, after which they are distinct through to the poly(A) tail. The CDNA can be used to express recombinant fibulin in a host cell. Fibulin binds to the receptors in a cation-dependent, EDNA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the protein have important diagnostic and therapeutic uses.

Claiminh, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.

See also Q11008 and Q11010.
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified fibulin, DNA encoding it and antibodies reactive with it
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Pred. No. 1.36e-05;
0; Mismatches 34; Indels
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370 attgatgaatgtgcctctggtaaagtcatctgtccctacaa 410
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/*tag= b
/product= fibulin B
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/label= point c
2505..2510
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Q70465 standard; DNA; 114 BP.
Q70465;
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Q11009 standard; cDNA; 2555
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2.1%;
Best Local Similarity 66.3%;
Matches 67; Conservative
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18-AUG-1989; US-3957
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US-013416. US-176500.

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1038 tatctcggttgactgcagcttcaatcatgggatctgtgactggaaacaggatagagaa 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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/note= "this sequence represents 'Z'; Z can
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Q70466 standard; DNA; 114 BP.
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05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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0; Gaps

Length 114;

Score 32; DB 12; Length 114; Pred. No. 4.97e-05; 30; Mismatches 70; Indels

2.0%;

Local Similarity

Conservative

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Terbuis noise, noise.

Per scening a recombinant vector library expressing fusion proteins of screening a recombinant vector library expressing fusion proteins of screening a recombinant vector library expressing fusion proteins of screening a binding domain and an effector domain proteins bisclosure; Page 35; 255pp; English.

C 70466 is a generic DNA sequence used to generate random TSAR (Totally crepresented as follows/KNNB)[TGC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) crepresented as follows are shown in R65151-54. TSARs are concernated by these generic sequences or peptides, comprising at least two functional regions - a binding commin with affinity for a ligand and a second effector peptide portion linker peptide between the 2 domains. The oligonouslectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues confer some degree of conformational rigidity to the peptides. The TSARs or companis, on peptide, toxin or beneficied or variant residues. These cresidues confer some degree of conformational rigidity to the peptides. The TSARs or companis, on beneficied and therefore circumvent the need for monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing creating the creaming the period or the repression of macromolecules.
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                                                                                                                                              31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                         WPI; 94-279739/34.
P-PSDB; R65152.
                                                                                                                                                                                                                           Fowlkes DM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be and represented as follows: X(NNB)6(TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are Comptend of the service of the same as Y) that are Comptend of the service of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins Disclosure; Page 35; 255pp; English.
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                                                                            /note= "this sequence represents '2'; 2 sequence of 6, 9 or 12 nucleotides (see
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Pred. No. 4.97e-05;
32; Mismatches 76; Indels
55..60
/*tag= a
/note= "this s
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                           comments)"
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larity 3.6%;
Conservative
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P-PSDB; R65150 and R65151.
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US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay BK;
                                                                                                                                                                                                                                                                                                                   30-DEC-1993;
                                                                                                                                                                        WO9418318-A
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Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; Synthetic rapid; detection; screening; treatment; generic; ss.
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31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
FOWLKES DM, Ray BK;
WPI; 94-279739/34.
P-PSDB; R58378.
Identifying proteins or peptide(s) which bind a ligand - by
69 bnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                  ctcgcaggettcgctctatgtcattcttcagggctttctcttc 892
                                                                                                                                                                                                                    /note= "encoded by 2 (see comments)"
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070470 standard; DNA; 114 BP.
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01-FEB-1994;
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                                                                                         970470;
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WO9418318-A.

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represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8 -(CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. The peptides generated by this and other generic sequences (070471-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated
                                                                                                                                                                                                                                                                                                               heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of marcomolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 5 A; 10 C; 0 G; 0 T;
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Q70473 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)3(CAC)(NNB)3(CAC)(NNB)3(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)3(CAC)(NNB)3(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(CAC)(NNB)6(C
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                              comprising a binding domain and an effector domain
Disclosure; Pageg 36; 255pp; English.
070470 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
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expressing fusion proteins
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Pred. No. 1.79e-04;
28; Mismatches 68; Indels
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC.) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI: 94-279739/34.
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Q70473 standard; DNA; 114 BP.
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affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARS or composes. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monocional or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARS are easily
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ative 25; Mismatches 64; Indels
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Sequence 114 BP; 8 A; 16 C;
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Search completed: Sat Apr 24 23:20:00 1999 Job time : 273 secs.

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在这个事情,我们也是我们的人,我们也是我们的人,我们们的人,我们们的人,我们们的人,我们们的人,我们的人,我们们的人,我们们的人,我们们的人,我们们的人,我们们	(ME)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 2350.24 Seconds 1227.509 Million cell updates/sec - n.a. database search, using Smith-Waterman algorithm Sat Apr 24 22:35:35 1999; n.a. srch_nn Run on:

Tabular output not generated.

>US-08-968-800-2 (1-1611) from US08968800.seq 1607 Description: Perfect Score:

1 ggctggagaagaaacagcaa......aattactagctgaaaaattg 1611 ccgacctcttctttgtcgtt......ttaatgatcgactttttaac N.A. Sequence: Comp:

TABLE default Gap 6 Gap Scoring table:

Dbase 0; Query 0 STD Nmatch 2275026 seqs, 895388244 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est56 Database:

l:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
3:enbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:qb_est15 12:gb_est16 13:qb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est2 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4 Database:

Mean 11.687; Variance 2.100; scale 5.565 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COMMENT

SUMMARIES

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No.	0.00e+00	00+00	00e+00	e+00	e+00	0.00e+00	e+00	00e+00	00e+00	.00e+00	.00e+00	.00e+00	00e+00
Pred. No	0.00	0.0	0.00	0.00	0.00	0.0	0.0	0.00	0.00	0.0	0.00	0.0	0.0
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/organism="Homo sapiens"
//orde="Organ: mixed (see below); Vector: pT7T3D-Pac
//hote="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three

source

FEATURES

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1094 Std Error: 0.00
High quality sequence stop: 477.

Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

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a; Hominidae;	Chordat Thini;	yotes; Meta Primates;	rial Euth	co.	EST. human. Homo sapiens Eukaryotae; Vertebrata;	SM	KEYWOR SOURCE ORGA
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	Homo sapien Soares preg Homo sapien Homo sapien	y140101.11 y150907.r1 z133c11.r1 y133b06.r1 y121d02.r1	10		, , , , , , , , , , , , , , , , , , ,		ਾ ਹਾ ਹਾ ਹਾ
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1.58e-140 2.06e-119 1.00e-100	Soares_feta Soares feta Soares feta	ow69c06.s1 ze83d06.s1 ze85d03.s1	AI023885 AA009486 AA025548		.υ.4 		
9.47e-230 5.66e-188 2.90e-179	Soares feta Soares_NFL_ Soares_feta	zj29e09.sl ol34a06.sl oz06d10.xl	AA707654 AA913032 AI057014		8.7.		
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Query Match
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AUTHORS
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normalized libraries (melanocyte 2NDHM, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA reaction. The driver was PCR-amplified CDNAs from pools 6,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, /db_xref="taxon:9606" (5000 clone="taxon:9606" clone="taxon:9606
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                                                                                                                                                                                                                            /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1092 agaagatgattttgactggaatcctgctgatcgagataatgctatttggcttctatatggc 1151
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Pred. No. 0.00e+00;
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ilarity 97.1%;
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// Angles of the control of the cont
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 403.
Location/Qualifiers
1. 508
//crgamism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoffae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheris; Primates; Getarihini; Hominidae; Home, 1 to 508; To 508; Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkln,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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0; Mismatches 15; Indels
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/clone="365765"
/clone_lib="Soares fetal heart NDHH19W"
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/dev_stage="19
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Local Similarity 96.2%;
les 487; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
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300

508 bp mRNA EST 14-AUG-1996 Soares fetal heart NbHH19W Homo sapiens cDNA clone

AA025649 508 bp ml 2e85d03.rl Soares fetal he 365765 5', mRNA sequence. AA025649

DEFINITION

ACCESSION

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Gaps

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Length 472; Indels

Score 438; DB 6; Le Pred. No. 0.00e+00; 0; Mismatches 9;

240

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419

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human clone=201021 primer=M13RP1 library=Soares fetal liver spleen
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 446)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rudaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                   1054 agetteaateatgggatetgtgactggaaacaggatagagaagatgattttgaetggaat 1113
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                                                                                                                                                                                                                                                                                                                                                        182 IGTTIGCTCTTIGATIACCGGCTGGC-GNAGACAAAGTCGAGAAACTTCGAGTGTTTGTG
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                                                                                                                  3 AGCTICAATCAIGGGATCIGIGACTGGAAACAGGAIAGGAGAAGAIGAITTIGACIGGAAT
                                                                                                                                                                                               63 CCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCCGGCCTTGCGAG-TCAC
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WashU-Merck EST Project
Washington University School of Medicine
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                                    Query Match 27.3%;
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/organism="Togan: mixed (see below); Vector: pT7T3D-Pac
/note="Crgan: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NDHPU, and fettal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones ande from the same 3 libraries. The pools
consisted of I.M.A.6.E. clones 260232-265223,
340488-345479, and 484488-489479."
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ler1a; Primates; Catarrhini; Hominidae;
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                                                         This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 441.
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1045 gttgactgcagcttcaatcatgggatctgtgactggaaacaggatagagaagatgatttt 1104
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Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Wash U-Merck EST Project 1997
                                        GACTGGAATCCTGCCTGATCGAGATAATGCTATTGGCTTCTATATTGGCAGTTCCGGCCT
                                                                                                                    TGNAAGGTCACAAGAAAAACATTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCC
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                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/tissue_type="Pooled human me]
pregnant uterus"
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 326
Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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WashU-Merck EST Project
WashU-Merck EST Project
WashU-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: 486 1810
Email: 586 1810
Email: 586 Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Riffin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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larity 96.8%;
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cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not it and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
High qality sequence stops: 314
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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1 (bases 1 to 411)
Hillidr,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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501, St. Louis, MO
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medi.
4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1810
Fax: 314 286 1810
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llarity 95.8%;
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20-JUN-1995

454 bp mRNA EST Homo sapiens cDNA clone 151568 3'

H03936 Yj44a05.s1 F H03936

DEFINITION ACCESSION

LOCUS

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double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not in and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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Deuterostomas, Chordata, Vertebrata, Gnathostomata, Osteichi
Sarcopterygii, Choanata, Tetrapoda, Amniota, Nammalia, Theri
Butheria, Archonta, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 454)
Hillier,L., Clark, N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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8501, St. Louis,
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
Washington University School of
4444 Forest Park Parkway, Box 85
Tel: 314 286 1800
Fax: 314 286 1810
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High qality sequence stops: 354
Source: IMAGE Consortium, LLNL
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/Organism="Homo sapiens"
/Oote="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Ist strand cDNA was primed with a Not I: oligo(dT) primer [5/double-stranded cDNA was size selected, ligated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Adjected with Not I and cloned into (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Same fetus as the fetal lung library, Soares fetal lung ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1276 Std Error: 0.00
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                                                                                             AAUU9900 429 bp mRNA EST 01-FEB-1997
2683d06.r1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
365579 5', mRNA sequence.
                                                                                                                                                                                                                                         Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 429)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Waterston, R., Williamson, A., Wohldmann, F., Trevaskis, E., WashU-Merck EST Project
Unpublished (1995)
805 gagatagtttccagaggcgggaactctcatggaggtaaaaaagggaatgaagagaaaatg 864
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 2; Indels 1
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/clone="36559"
/clone=lib="Soares fetal heart NDHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)
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High quality sequence stop: 372.
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WashU-Merck EST Project
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Best Local Similarity 96.8%;
Matches 399; Conservative
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cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteichthyes;
.a; Theria;
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CGAA-CCTGCGAAGAAGATGTGTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTG 179
                                                                                                                                                  240 GGTTGACTGCAGCTTCAATCATNGGGATCTGTGACAGGAAACAGGATAGACGAAGATGAT 299
                                                                                                                                                                                                                                TTTGACTGGAATCCTGCTGNTCGAGATAATGCTATTNGGCTTCTATATGGCAGTTCCCGG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                 180 ATTCTCGGTCCAAAGGAAAGCGCTAACTTCCAAACTGGAACATAAAGATTTAAATATCTC
                                                                                                                                                                                                                                                                                                                               360 CCTTTGGCAGGTCCACAAGAAAGACATTTGGCCCGATTTGAAACTTCTCCTA 411
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Eax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 292
Source: IMAGE Consortium, LLNL
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The WashU-Merck EST Project
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1 (bases I to 442)
Hillier,L., Clark, N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human clone=21599 library=Soares infant brain 1NIB vector=Lafmid BA
                                                                                                                                                                                                                                                  1429 aaaaccggcgaaatcgcagtggatggcgtcttgcttgtttcaggcttatgtccagatagc 1488
                                   taccggctggccggagacaaagtcgggaaacttcgagtgtttgtgaaaaaaagtaacaat 1308
                                                                                                            1309 gccctggcatgggagaagaccacgagtgaggatgaaaagtggaagacagggaaaattcag 1368
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                                                                                                                                                   TIGIAICAAGGAACIGAIGCIACCAAAAGCAICAITITIGAAGCAGAACGIGGCAAGGGC 180
                                                                                                                                                                                                                                                                                                         CTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTCAGTTCC 300
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                                                                                                                                                                                                                              181 AAAACCGGCGAAATCGCAGTGGATGGCGTCTTGCTTTCTTCAGGCTTATGTCCAGATAGC
                                                                          GCCCTGGCATGGGAGAGACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAG
 TACCGGCTGGCCGANGACAAAGTCGGGAAACTTCGAGTGTTGTGAAAAACAGTAACAAT
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Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
High qality sequence stops: 305
Source: IMAGE Consortium, LLNL
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modifiled pT773 vector. Library went through one round of normalization. Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 75 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 372.
Location/Qualifiers
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
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(db_xref="taxon:9606"
                                                                                                 126 AAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGGAACCCACCAGGGNTCCTACCCCTAAG
                                                                                                                                                                                                                                                                                                                                                                186 GIGAACTIGCAGCCCTICAACTAIGAAGAGATAGTITCCAGAGGCGGGAACTCTCAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 GGTAAAAAGGGAATGAAGAGAAATGAAAGGGGGCTTGAGGATGAGAAAAGAGAAAGA
                                                                        306 AAAGCCCTGAAGGATTGACATAGGAGGGAGCGACCTTTTCGAGGGAGATGTTTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1674607"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
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/lab_host="DH10B (ampicillin resistant)"
                           Indels
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AI057064
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Mismatches 11;
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Similarity 95.8%; 345; Conservative
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                                                                                                                                     162 CAGGGAACTGACATACAAAGTCAAATATAAAGATAGTAACATTCAGTCATCCACAGATAA 221
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 884 Std Error: 0.00
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  24 pp mRNA EST 17-OCT-1996 2600004.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone W80921 5', mRNA sequence.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                       222 AAGGCIATCTGGACATAAGCCTGAAACAAGCAAGACGCCATCCACTGCGATTTCGCCGGT
                                                                                                                                                                                                                                                                                           342 CAACTGAATTTICCCTGTCTTCCACTTTTCATCCTCACTCGTGGTCTTCTCCCATGCCAG
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                                           Length 406;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
WashU Werck EST Project
WashU Worron University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                                     Score 296; DB 18; L
Pred. No. 0.00e+00;
0; Mismatches 6;
  126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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High quality sequence stop: 302,
Location/Qualifiers
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  65
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                                      18.4%;
98.0%;
                               Query Match 18.4%;
Best Local Similarity 98.0%;
Matches 299; Conservative
86
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutherla; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 347)

1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trieverskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot - 5. Library constructed by M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung library.
                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AACAGTAACAATGCCCTGG-ATGGGAGAAGACCACGAGTGAGGATGAAAAGTGGAAGACA 178
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                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                     Length 344;
                                                                                                                                                                        /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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/clone=335719"
/clone=1b="Soares fetal heart NbHH19W"
/sex="unknown"
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Pred. No. 0.00e+00;
0; Mismatches 8;
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Local Similarity 95.7%;
les 331; Conservative
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Source: IMAGE Consortium, LLML
This clone is available rogaty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                               GGCAGGTCACAAGAAGACATTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCCA 180
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1 (bases 1 to 374)

Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucabb,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Contact: Wilson RK
WashU-werck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                 3 others
                                                                                                                                                                                                                                       Length 347
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R27678
9783813
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Pred. No. 0.00e+00;
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ilarity 95.9%;
Conservative
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ACCESSION
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AUTHORS
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cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ë,
                                     Contact: Wilson RK
WashUrwerck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 242
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (inf@eimage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1356 agggaaaattcagttgtatcaaggaactgatgctaccaaaagcatcatttttgaagcaga 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1296 aaacagtaacaatgccctggcatgggagaagaccacgagtgaggatgaaaagtggaagac 1355
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1 (bases 1 to 364)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hulthan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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YA46602.r1 Homo sapiens cDNA clone 132794 5'
827153
9783288
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                           116
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63 c 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity 95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.9%;
Matches 280; Conservative
Unpublished (1995)
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```

```
Contact: Wilson RK
Washbrack EST Project
Washbrack Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@waston.wustl.edu
High quality sequence stops: 283
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                  1495 tctgtgg-annnctgaatggtactatctttatatttgactttgtatgtccagttccctggt 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TCTCTGGGATGACTGAATGTTACTATTTATATTTGACTTTGTATGTCAGTTCCCTGGT 240
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Pred. No. 0.00e+00;
0; Mismatches 5; Indels
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                                                                                                                                                             Location/Qualifiers
1.364
//Organism="Homo sapiens"
/Clone="132794"
a 56 c 95 q 111
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Cest Local Similarity 96.5%;

Atches 281; Conservative
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